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AG033781 Pan trog1
AI598135 tn14a10.x
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BASE COUNT	COMMENT CC TI TI C C C C C C C C C C C C C C C C	SE SM	RESULT 1 B1087886 LOCUS B1 DEFINITION 60 ACCESSION B1 VERSION B1 KEYWORDS ES		C 42 331.2 C 43 330 C 44 328.8 C 45 318.8
/organism="Homo sapiens" /db_xref="taxon:9606" /db_xref="taxon:9606" /clone="mAGE:4993894" /clone=lib="NHI_MGC_10" /cell_line="MGC36" /lab_host="DH10B" /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.5 kb. Library prepared by Life Technologies." 225 a 206 c 166 g 174 t	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nlh.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://inagge.llnl.gov Plate: LLAM11015 row: d column: 23 High quality sequence stop: 762. L.Cation/Qualifiers 1771	human. hu	BIO87886 771 bp mRNA linear EST 20-JUN-2001 602852690F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4993894 5', mRNA sequence. BIO87886 BIO87886.1 GI:14506216	ALIGNMENTS	52.2 471 9 AA709471 . 52.0 569 12 AQ580978 51.8 438 10 R77278 50.2 840 12 AQ893377
MV-SPORT6; Site_1: NotI; nally. Primer: Oligo dT. ary prepared by Life	ies, Inc. , Inc. on information can be LNL at:	Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. nci.nih.gov/. of Health, Mammalian Gene Collection (MGC)	linear EST 20-JUN-200: clone IMAGE:4993894 5',		AA709471 zf91h06.5 AQ580978 RPCI-11-4 R77278 y175d06.s1 AQ893377 HS_3072_A

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Pan troglodytes DNA, clone: PTB-130M15.F

AG121669

AG121669.1 GI:16650834

GSS; GSS (genome survey sequence).

Pan troglodytes male lymphoblast DNA, cl

BAC Library clone:PTB-130M15.F.

Pan troglodytes

Pan troglodytes
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570; Conserv
         Fujiyama,A., Hattori,M.,
Totoki,Y., Watanabe,H. a
                             BAC end sequences
Unpublished
2 (bases 1 to 689
                                                         Fujlyama, A., Hattori, M., To
Totoki, Y., Watanabe, H. and
                                                                                         Mammalia; Eutheria;
                                                                                                  Eukaryota; Metazoa;
                                                                               (sites)
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  Submission
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Pred. No. 7.7e
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nd Sakaki,Y.
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nd Sakaki, Y.
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Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
/clone_lib="PTB Thimpanzee Male
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    254
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                                                                                                                                                                                                                                   131 ctgctagcccatgctccgatgttaatgacattgaaggcacccctcccgaggaaatctcaa 190
                                                                                                                                                                                                                                                                                             Local
ctgcacaacccctactatgccccaattcagcgggaagcagttagagcggtcatcagccaa 250
                                                   CTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGCACCCCTCCTGAGGAAATCTCAG 435
                                                                                                          CCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAGACAGGACTAGCT 315
                                                                                                                                                                 CTGCACAACCTCTACTACGCCCCAATTCAGCAGGAAGCAGTTAGAGCGGTCGTCGGCCAA 375
                                                                                                                                                                                                                                                                              458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1645 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 475.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 494)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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AA781423
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similar to
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                                                                                                                                                                                                                                                                                                                                                               108
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                         Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 111 c 133 g 141 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="1391428"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                        68.8%;
92.7%;
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Primates;
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Pred. No. 1.6e-82;
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                Email: johnq@tigr.org
Plate: 292
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91.8%;
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522 AGGTTTAAGATCTTCCGCGGACCCCTAAAACTGGCTTGCTAGCCCATGTTCTGGTGTTAA 463
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cctgttgagaggggggactgagagacaggactagctggatttcctaggccaacgaagaat 334
                                                                                            attcagcgggaagcagttagagcggtcatcagccaacctccccaacagcacttgggtttt 274
                                                                                                                                                                     tgacattgaaggcacccctcccgaggaaa-tctcaactgcacaacccctactatgcccca
                                                                        GTTCAGCAGGAAGCAGTTAGAGTGGTCATCAGCCAACCTCACCAACAGCACTTGGGTTTT 343
                                                                                                                                                 TGACATCGAAGTCACTCCTCCTGAGGAAATTCTCAACTGCACAACCCTTATTATGCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 3528
Fax: 301 838 0208
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EST383642 MAGE resequences, MAGL Homo sapiens
AW971553
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Hegde,P., Qi,R., Abernathy,K., Dharap,S.,
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assessment of gene expression patterns in a model metastasis using a 19,200 element cDNA microarray
                                                                                                                                                                                                                                                                                                                                                                                                              Score 432.4; DB
Pred. No. 1.5e-81
0; Mismatches 4
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                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes DNA, clone: PTB-008021.F, genomic survey sequer AG033781.
AG033781.1 GI:16560654
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee BAC Library clone:PTB-008021.F.
                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama, A., Hattori, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                  LIBRARY
                                                                                                                                                                                                                                                                                                           lone tracking errors.
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R.Site 1 : SacI
R.Site 2 : SacI.
 Conservative
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                                                                                  /clone="PTB-008021.F"
/sex="male"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
/clone_lib="PTB Chimpanzee Male
155 c 178 g 173 t
                                                                                                                                                             /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                      ocation/Qualifiers
               66.6%;
88.0%;
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 0,
               Score 423; DB 12;
Pred. No. 1.3e-79;
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nd Sakaki, Y.
Mismatches
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genomic
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RESULT 6
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                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 490)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
             CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                    Bonaldo,
                                                                                                                                Ph
                                                                                                                                             Tissue Procurement: David N. Louis,
                                                                                                                                                                        Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                    Homo sapiens
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           Insert Length:
                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                     (CGAP/BTGAP),
primer:
                                                                                                                                                           cgapbs-r@mail.nih.gov
                                                                                                    Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                      490 bp mRNA linear EST 12-MAY-1999 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167578 3' contains PTR5 tl PTR5 repetitive element;, mRNA
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    -40UP
                                                                                                                                                                                                     Tumor Gene Index
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                                                           information
                                                                       Sequencing Center
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 440)
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601571305F1 NIH_MGC_21 Homo
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                                                                                  mRNA sequence.
                                           human.
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35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Brn25"
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                                                               GI:10146665
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92.9%;
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Pred. No. 4.9
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Mismatches 33;
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CTATTAAATCTTGCAACTG 439
                                                                                                                  CCACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTGACCAATCAGAGAGC
                                                                                                                                                                                                                                             TGAGAGCACAGCAGGAGGACAATGATCGGGATATAAACCCAAGTCTTCGAGCCGGCAAC
                                                                                                                                                                                                                                                                  tgagagcacagcgggagggacaaggatcggggatataaacccaggcattcgagccggcaac 538
                                                                                                                                                                                                                                                                                                                                                            TCACTAAAATGCTAATTAGGCAAAGACAGGAGGTAAAGAAATAGCCAATCATCTATTGCC
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National Institutes of Health, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="choriocarcinoma"
/lab_host="DHIOB (phage resistant)"
/note="organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.

Birectionally cloned into EcoRI/XhoI sites using the placetionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCAGGAGG(). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

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/clone_lib="NIH_MGC_21"
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/db_xref="taxon:9606"
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Pred. No. 3.9e-74;
0; Mismatches 26;
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                                                                             Local Similarity
nes 467; Conserv
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Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lemishka,I., Scearce,M., Brestelli,J., Gradwohi,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
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BI963185
BI963185.1 GI:16337590
EST.
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Library was constructed by Dr. Douglas Melton DNA sequencing by
Washington University Genome Sequencing Center For information
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Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               obtaining a clone please contact: Juliana Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (brown@fas.harvard.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 543)
                                                                                                                                                                                                                                                                                                                                                                             116
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 451.
                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by Oilgo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
                                                                                                                                                                                                                                                                                                                                                                             Ø
                                                                                                                                                                                                                                                                                                                                                                           by hydroxyapatite chromatography and used library."
123 c 147 g 156 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Islets of Langerhans"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Both"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Melton Normalized Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
                                                                                                                                                                                                                                                                  62.4%;
                                                                                                                                                                                                                                                 Score 396; DB 10;
Pred. No. 7.2e-74;
0; Mismatches 51;
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                                                                                                                                                                                                                                                   51;
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Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                        Length 543;
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AG058970/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aacatggggcttgcaacttagctcacacccgaccaat-----cagagagctcacta 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACAAGGGGGGGACAATGATCAGGATATAAACTCAGGCATTCAAGCCAGCAATGGCTAC
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                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS; GSS (genome survey sequence)
Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-046A08.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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AG058970
AG058970.1 GI:16596431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AG058970
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R.Site
                                                                                                                                                                                                                                                                                          Vector
                                                                                                                                                                                                                                                                                                                                                                       tracking errors.
                                                           /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
/clone_lib="159 g 191 t
                                                                                                                                                                                                           1. .651
                                                                                                                                        /clone="PTB-046A08
                                                                                                                                                                                 /organism="Pan troglodytes"
                                                                                                                                                              /db_xref="taxon:9598"
                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metazoa; Chordata; Craniata; Ve
Sutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                     : pKS145
: SacI
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clone_lib:PTB Chimpanzee Male

GSS 02-NOV-2001

126

186

373

Vertebrata; i; Hominidae;

Euteleostomi;

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CCESSION VERSION KEYWORDS
                    COMMENT
                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
AG126669/c
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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccctttgggtcccctccctttgtatgggcgctct 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCTTTGGGTCCCCTCCCATTGTATGGGAGCTCT
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Pan troglodytes DNA, clone: PT
AG126669 1 GI:16655834
GSS (genome survey sequen
Pan troglodytes male lymphobla
BAC Library clone:PTB-137E19.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAGTGGGAGGACAATGGTCGGGGTATAAACCCAGGCATTCGAGCAGGGAGTGGCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                503;
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC ence was generated during the R&D process and may have higher chance of
                                                                                                                  Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                      Fujiyama, A., Hattori, M.,
                                                                                                      Direct Submission
                                                                                                                                                           Unpublished
                                                                                                                                                                                      Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                Eukaryota;
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                                                                                                                                                                                                                     (sites)
                                                                                                                                            (bases 1 to 701)
                                                                                                                                                                          end
                                                                                                                                                                                                                                                                           ; GSS (genome survey sequence).
troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee
Library clone:PTB-137E19.F.
                                                                                                                                                                                                                                                               troglodytes
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                                                                                                                                                                            sequences
                                                                                                                                                                                                                                              Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.2%;
87.6%;
                                                                                                                                                                          of Library
                                                                                                                                                                                                                                   Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 394.8; DB 1
Pred. No. 1.2e-73;
D; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                1 bp DNA PTB-137E19.F,
                                                                                                                                                                                                                                Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
                                                                                                                               Taylor, T.D., Yada, T.
                                                                                                                                                                                                      Taylor, T.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                Vertebrata;
                                                                                                                                                                                                                                                                                                                                               linear
genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                               04-NOV-2001
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                                                      Pan troglodytes DNA, clone: PTB-056L1s
AG066901
AG066901.1 GI:16618703
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone: PTB-056L15.F.
                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                              Pan troglodytes
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Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae

Hominidae;

Euteleostomi;

clone_lib:PTB

Chimpanzee

Male

609 bp DNA clone: PTB-056L15.F,

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/clone_lib="PTB Chimpanzee
/close_182 g 195 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="PTB-137E19
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88.1%;
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Pred. No. 2.6e-73;
Pred. No. 2.6e-73;
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             acccaggcattcgagccggcaaccgccaaccccctttgggtccccttccctttgtatgggcg
                                                                 gaaatagccaatcatctattgcctgagagcacagcgggaggagagaggatcggggatataa
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                                                                                                                                                                                                                                                                                                                                     aaactgtaaaactacaaattgttcttcaaatggagcaccagatggagtccatgactaaga 106
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                                                                                                                                                                                                                                                                                                                         AGCCCCTTCTCCCAAGGAAATCTCAACTGCACCACCCCTACTACACCCCAATTCAGCAGG
                                                                                                                                                                                                                                                                                                                                                                        TCTACTGCAGACCCTTGGACCAGCCTGCTAGCTCATGCTCCAAATGTTAATGGCCTTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel:81-45-503-9111, Fax:81-45-503-51.v,
Clones are derived from the chimpanzee BAC library PTB This BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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/clone_lib-"PTB Chimpanzee Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-056L15.F"
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87.7%;
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nd Sakaki,Y.
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome

Clone distribution: NCI-CCAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1375 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Louis M. Staudt, M.D., Ph.D., Ph.D., Gerald Marti, M.D. cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST.
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od26b10.s1
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Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1369051"
/clone_lib="wCI_CGAP_GCB1"
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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                                                                                                                     Score 392.6; DB Pred. No. 4e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HS_3131_B2_E04_MR CIT Approved Human Ge sapiens genomic clone Plate=3131 Col=8 AQ892947
                                                                                                                                                                                                                High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3131 row: J column: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ892947.1 GI:6349137 GSS.
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                                                                                                                                                                                           Seq primer: Ml3 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                              Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                    161
                                                                                                                                                                 quality sequence stop: 712
Location/Qualifiers
                                                              /note="Organ: sperm;
E-Coli DH10B"
                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=3131 Col=8 Row=J"
/clone_lib="CIT Approved Human Genomic Sperm Library
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8 Row=J, DNA sequence.
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                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
Insert Length: 720 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 436)
                                                                                                                                                                                                                                                                                                                     AI128526
AI128526.1
                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                        Homo sapiens
                                         quality sequence stop: 428.
Location/Qualifiers
                                                                                                                                                                               Gene Index
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                      GI:3597040
                                                                                                                                                                                                                                          Chordata;
Primates;
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Mismatches 94;
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Catarrhini;
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i; Hominidae;
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AUTHORS
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Best Local Similarity
Matches 403; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTAGGTTTTCCTGTTGAGATGGGGGACTGAAAGACAGGACTAGCTGGATTTCCTAGGCTG
Tumor Gene Index
Unpublished (1997)
Contact: Robert St
                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae, 1 (bases 1 to 446), NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NRIJORAL Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                      A1393478 446 bp m

1945904.x1 Soares_NFL_T_GBC_S1 Homo

IMAGE:2111766 3', mRNA sequence.

A1393478

A1393478.1 GI:4223025
                                                                                                                Homo sapiens
                                                                                                                              human
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M.Fatima Bonaldo."
a 96 c 106 g 139 t
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/clone-lib="Soares_placenta_8to9weeks_2NbHP8to9w"
/clone-lib="Soares_placentae: one from 8 weeks and ai
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.9%;
93.7%;
 Strausberg,
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                                                                                    Hominidae;
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s cDNA clone
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                                          Project (CGAP),
                                                                                                 Euteleostomi;
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                atccacctctaaacatggggcttgcaacttagctcacacccgaccaatcagagagctcac 422
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                                                                                                                                                                                                                                                                                    Seq primer: -400r ..... 445.
High quality sequence stop: 445.
Location/Qualifiers
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1061 Std Error: 0.00
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:2111766"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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92.5%;
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Pred. No. 1.4e-71;
0; Mismatches 24;
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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   Score
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Match
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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    US-09-319-156A-6
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US-09-078-294-4
US-09-078-294-3
US-08-691-563C-58
US-08-691-563C-58
US-08-464-051-1
US-08-462-498-1
US-08-462-498-1
US-08-462-498-1
US-08-462-498-1
US-08-54-385-2
US-09-247-155-42
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1 2323 61 2383 121 2431 181 2491 2491	Sequence 3, Patent No. (GENERAL INFO APPLICANT: APPLICA	22255555555555555555555555555555555555
cccty ccaaat caaat ctgga ctgga ctggaaat gaaat catca cgtcg		300.000.000000000000000000000000000000
tcaacc ccaacc	3, Application US/ 0. 6312921 INFORMATION: NT: JACODS, Kenneth NT: MCCOS, John M. NT: LaVallie, Edwar NT: Cavallie, Edwar NT: Evans, Chery! NT: Treacy, NT: Treacy, NT: Genetics Instit FINVENTION: SECRET FERRICE: 6006B, AJT; FAPPLICATION NUMBER FILLING DATE: 1998- OF SEQ ID NOS: 62 E: Patentin Ver. 2. 03 03 03 03 03 03 03 03 03 03 03 04 05 08 08 09 08 09 09 09 08 09 08 09 08 09 08 09 09 09 09 09 09 09 09 09 09 09 09 09	444444444444444444444444444444444444444
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thaagtttgtctctt	15928A A. A. A. PROTEINS AND POLYNUCLEO 5/09/175,928A 0 Score 533.8; DB 4; Pred. No. 5.9e-162; 0; Mismatches 42;	US-08-847-429A-8 US-09-065-474-8 US-09-065-474-8 US-08-706-214-1 US-09-031-485-32 US-09-031-485-32 US-09-031-485-32 US-09-031-485-32 US-09-065-474-32 US-08-847-429A-34 US-08-30-518-1 US-08-330-283-1 US-08-330-331-1 US-08-895-522-2 US-09-195-331-2
ctgtaaaacta ctgtaaaacta ctgtaaaacta accgtggaccc	ENCODING h 2946; s 12; G	Sequence 8, Sequence 8, Sequence 1, Sequence 32, Sequence 34, Sequence 34, Sequence 34, Sequence 31, Sequence 1, Sequence 2, Sequence 3, Sequence 2, Sequence 3, Sequence 2, Sequence 2, Sequence 3, Sequence 2, Sequence 3, S
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                                           ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-8851

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 279 base pairs

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5/00-170N:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikil
TITLE OF INVENTION: ENCODING TF
TITLE OF SEQUENCES: 71
                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,878A
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APPLICANT:
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MEDIUM TYPE: Floppy
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MOLECULE TYPE:
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CITY: C
                             TYPE: nucleic
STRANDEDNESS:
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                TOPOLOGY:
                                                                                                                                                                                                                                              FILING DATE:
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                              double
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US-08-721-489-4
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Best Local Similarity
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APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED P
TITLE OF INVENTION: ENCODING T
NUMBER OF SEQUENCES: 5
                                                                                             TELEFAX: (617) 876-58 INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/721,489
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                            SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418
                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 87 Cambi
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                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RCCACATCCACCTTTAAACACGGGGNTTGCAAANAAGATNACACTTGACCAATCAGAGAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTCANTAAAATGATNATTNGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTATTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctcactaaaatgctaattaggcaaaaataggaggtaaagaaatagccaatcatctattgc 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGCAACCCCTTTGGGTCCCCTTCCCTTTGTATGGGAGCTNTGTTTTCATGCTATTTCAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
TYPE:
                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                      E: Genetics Institute,
87 CambridgePark Drive
                                                           279 base pairs
                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McCoy, John
LaVallie, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobs, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Racie, Lisa
                linear
                                                                                         7) 430
3 876-5851
- NO: 4:
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88.1%;
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Pred. No. 7.6e-66;
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US-08-691-563C-46
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                                                                                                                            FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: BETTIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                 TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563C
FILING DATE: 02-AUG-1996
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Oliff & Berridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: THERAPEUTIC PURPOSES
TITLE OF INVENTION: THERAPEUTIC PURPOSES
                  MOLECULE TYPE:
                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Colette JOLIVET
APPLICANT: Bernard MANDRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                 STREET: 700 South
CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
                                                                        LENGTH:
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                                                                                                                     703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frederic BESEME
Frederic BEDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herve PERRON
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88.1%;
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                                                                                                                                                               WPB 38588
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Pred. No. 7.6e-66;
1; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                               Street,
                                                                                                                                                                                                                                                                                                                                                                                               Suite 300
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gaaatctcaactgcacaacccctactatgccccaattcagcgggaagcagttagagcggt 240

gacactaccactgcagggccccttcttcaccccctatccagcaggaagtagctacagcggt 59118

59008

ctggaccgacccgctggccc-----

ctggaccggcctgctagcccatgctccgatgttaatgacattgaaggcacccctcccgag

tttcaatggcctaaagagctcccctctggag

180

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; LENGTH: 80246
; TYPE: DNA
; ORGANISM: Nucleotide sequence of NC-contig
US-09-078-294-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-078-294-4
                                                                                                                                                   Query Match 19.8
Best Local Similarity 67.2
Matches 213; Conservative
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09078294 Patent No. 6265211
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEO ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
  58948
                                                                              58888
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                                                                                            1 ccctgtatctttaacctccttgttaagtttgtctcttccagaatcaaaactgtaaaacta
                                                                          cctgtatttttaacctcttggtcaaatttgtttcctctaggatcgaggccatcaagcta
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cagatgatcttacaaatgtaaccccaaatgagctcaactaacaacttctgctgaggaccc
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62.7%;
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                                                                                                                                                     Score 125.8; DB 4;
Pred. No. 9.3e-30;
Pred. No. 9.3e-30;
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; Sequence 3, Application US/09078294

; Patent No. 6265211
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                                                     Sequence 58, Application US/08691563C
Patent No. 6001987
GENERAL INFORMATION:
APPLICANT: Herve PERRON
APPLICANT: Frederic BESEME
APPLICANT: Frederic BEDIN
APPLICANT: Glaucia PARANHOS-BACCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
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SEQ ID NO 3
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APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                    59241 ctggaccgacccgctggccc-----tttcaatggcctaaagagctcccctctggag 59291
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 APPLICANT:
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nes 213; Conservative
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                                      Frederic BESEME
Frederic BEDIN
Glaucia PARANHOS-BACCALA
Florence KOMURIAN-PRADEL
           Colette JOLIVET
Bernard MANDRAND
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 VIRAL MATERIAL AND
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0; Mismatches
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NUCLEOTIDE FRAGMENTS
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nes 92;
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                          CORRESPONDENCE ADDRESS
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             ADDRESSEE:
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US-08-232-463-14/c
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                                                                                                                     Sequence 14, Application Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-836-2787 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                            1026 CATCGGCCAA-ATTCCCAACAGCAGTTGGGGTGTCCTGTTTAGAGGGGGGGATTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                856 CAGATGGTCTTACAAATGGAACCCCAAATGAGTTCAACTAACAACTTCTACCAAGGACCC 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              796 CCCTGTATTTTTAAGCTTCTTGTCAAATTTGTTTCCTCTAGGATCGAAGCCATCAAGCTA 855
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                                                                                                                                         US/08232463
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Pred. No. 2e-30;
0; Mismatches
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Foley & Lardner 00 Diagonal Road,

Suite

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FOWLPOX VIRUS

COUNTRY: 114

USA

22313-0299 Alexandria

ADDRESSEE:

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US-08-011-398B-1/c
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                        GENERAL INFORMATION:
APPLICANT: Roger Brent
APPLICANT: Antonis S. Ze
TITLE OF INVENTION: MAX
TITLE OF INVENTION: MOLE
                                                                                                   Sequence 1, Application US/08011398B Patent No. 5512473
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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CLONE: pTZgpt-
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                      1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              1082 RRRRRRRRRRRRRRRATCGCAAGCTCCCTCG
                                                                                                                                                                                                                                                                                                                 1202
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PRIOR APPLICATION DATA:
               NUMBER OF SEQUENCES:
                                                                                                                                                                                                            521 ggcattcgagccggcaacggcaaccccctttg
                                                                                                                                                                                                                                                                                  461
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TELEX: 899149
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                                                                                                                                                                                                                                                      cccgaccaatcagagagctcactaaaatgctaattaggcaaaaataggaggtaaagaaat 460
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                          MAX-INTERACTING PROTEINS MOLECULES AND METHODS
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54; Mismatches
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                                           AND RELATED
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Best Local Similarity
Matches 57; Conserv
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                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                              ZIP: UZ110 200
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 50Z or 55SX
COMPUTER: MS-DOS (Version 5.1)
                        OPERATING SYSTEM: MS-DOS (Version 5 SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MEDIUM TYPE: 3.5" Diskette,
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                               APPLICANT: Roger Bren APPLICANT: Antonis S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             539 ggcaaccccctttgggtcccctccctttgtatgggcgctctgttttcactctatttcact 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 225 | CITY: Boston
                                                                                                                                 COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Paul T. Clark REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 29 JAN 1993
                                                                                                                                                               STATE:
                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                               ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
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APPLICATION NUMBER: US/0: FILING DATE: 05 JUN 1995
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Pred. No. 1;
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CLASSIFICATION: 435 RIOR APPLICATION DATA: APPLICATION NUMBER: 08/0 FILING DATE: 29 JAN 1993

08/011,398

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RESULT 11
US-08-462-498-1/c
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Matches
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55XX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 3.5" D1
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APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
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                                                                                                         NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
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STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                          CLASSIFICATION: 435
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Pred. No.
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; STRANDEDNESS: singl
; TOPOLOGY: linear
US-08-462-498-1
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US-08-554-385-2
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                                                                                 Query Match
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                                                                                                                                                                                                                TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
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                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0 SOPTWARE: Wordperfect (Version 5.1) CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
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APPLICANT: Antonis S.
TITLE OF INVENTION: MI
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                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                     LENGTH: 2417
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                               NAME: Karen F. Lech
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: No. 60
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                                                                     Local
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GGGAAGGCCTCTTGGAGACCTTACCCCTGGCTGTTTGGACTTTGTATACTTTAAATAATT 103
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6017692
                                                      1 Similarity
57; Conserv
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                                                        Conservative
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linear
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MAX-INTERACTING PROTEINS AND RELATED
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                                                     O; Mismatches
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Pred. No.
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                                                                                 DB 3;
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RESULT 14
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Matches
                                                                                       Sequence 1, Application US/08011398B Patent No. 5512473 GENERAL INFORMATION:
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EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1998-08-10 EARLIER APPLICATION NUMBER: 60/099,273 EARLIER FILING DATE: 1998-10-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: sig_peptide
LOCATION: 39. 83
OTHER INFORMATION: Von Heljne matrix
OTHER INFORMATION: score 4.6
OTHER INFORMATION: seq LLTHNLLSSHVRG/VG
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ORGANISM: Homo sapiens
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LOCATION: 583..598
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NAME/KEY: CDS
LOCATION: 39..413
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                APPLICANT: Roger Brent
APPLICANT: Antonis S.
TITLE OF INVENTION: MA
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MAX-INVERACTING PROTEINS AND RELATED

MOLECULES AND METHODS

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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Antonis S.
TITLE OF INVENTION: A
TITLE OF INVENTION: A
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                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
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PRIOR APPLICATION DATA:
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ADDRESSEE: Fish & Richardson
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                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Paul T. Clark
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                           OPERATING SYSTEM: MS-DOS (Version 5 SOFTWARE: WordPerfect (Version 5.1)
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TYPE: 3.5" Diskette, 50z or 55x
ER: IBM PS/2 Model 50z or 5.5
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Pred. No. 2.2e-187;
Mismatches 0;
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RESULT AAX29702

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid sequences of retrovirus called MSRV-1 multiple sclerosis or rheumatoid polyarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUL-1997;
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35; Conservative
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Pred. No. 2.2e-187;
Mismatches 0;
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The present sequence represents the nucleotide sequence corresponding to the 3' env region and long terminal repeat sequences from clone CL6 of Multiple Sclerosis retrovirus (SREV-1). The specification describes a long terminal repeat (LTR)-RU5 region which encodes the expression of a MSRV-1 protein. This is unusual for LTRs, in particular in the RU5 region. The sequence includes CAAT and TATA
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                   1756
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..2e-181;
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Multiple s gag gene;

sclerosis; env gene;

associated

retrovirus;

retrovirus; MSRV; MS; arthritis-associated

pol gene; virus; ss

rheumatoid

Multiple sclerosis

associated

retrovirus

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid from retroviruses - useful prevention and treatment of, e.g. multiple
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nilarity 92.4%;
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/transl_except=
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stop codon)
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stop codon)
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s-Baccala G, Perror
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xcept= (pos:77-79, appears
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Pred. No. 3.3e-159;
D; Mismatches 47;
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Matches 572
                                                                                                                                      related virus type 1 (MSRVI). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with
                                                                                                            Sequence
                                                                                                                              multiple sclerosis rheumatoid polyart
                                                                                                                                                                   This
                                                                                                                                                                                    Claim 1; Page 39-40;
                                                                                                                                                                                                     Nucleic acid sequences of retrovirus called MSRV-1 multiple sclerosis or rheumatoid polyarthritis
                                                                                                                                                                                                                                                                                                                                                   Multiple sclerosis related virus
                                                                                                                                                                                                                                                                                                                                                                     Multiple sclerosis; virus; di rheumatoid polyarthritis; ss.
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                                                               Score 545; DB 20;
Pred. No. 3.3e-159;
D; Mismatches 47;
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21-NOV-1997;
18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein; testes; brain; blood; placenta; human; murine; thymus; bone marrow; treatment; prevention; nutrition; cytokine; immune; vaccine; cell proliferation; cell differentiation; suppressor; tumour inhibition; haematopoiesis regulator; activin; inhibin; chemotactic; chemotinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth; ss.
                                                                                                                                                                                                                                                                              03-JUN-1999
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Query Match Best Local S Matches 581

Local Similarity nes 581; Conserv

84.18; ilarity 91.58; Conservative

Score 533.8; Pred. No. 1.5e 0; Mismatches

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polynucleotides isolated from human adult testes, adult brain, adult blood or adult placenta, or murine adult bone marrow or thymus cDNA clibraries. The products of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides are also stated to be useful or the polynucleotides 
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Best Local
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                                                                                                                                                                                                             treating, preventing or ameliorating medical conditions in humans and animals. Detection of the levels of the proteins can be used for the diagnosts of e.g. pre-eclampsia, placental pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested activities include nutritional activity (e.g. in feeds), cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopolesis regulating activity, tissue growth activity, activin/inhibin activity, chemokinetic activity, activin/inhibin activity, chemokinetic activity, anti-inflammatory activity, cablerin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotide sequences are also stated to be useful for gene therapy.
                                                2323
                                                                                                                                                                                                                                                                                                                                                                                                                   This is the human secreted protein AJ172_2 nucleotide sequence, obtained from a human adult testes cDNA library. The invention relates to secreted human and murine proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; disease diagnosis; pre-eclampsia; cancer placental pathology; metastasis inhibition; nutritional activity; immune stimulator; haematopolesis regulator; tissue growth; tumour inhibitor; anti-inflammatory; clone AJI72_2; ATCC_98115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 107-108; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding secreted cDNA libraries, used to develop products for the diagnosis and treatment of neoplastic disease
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caaattgttcttcaaatggagcaccagatggagtccatgactaagatccaccgtggaccc
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DB; AAY67313.
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                                                                                                                                                                                                                              Human endogenous retrovirus
                                                                                                                                                                                                                                                    Envelope protein; HERV; syncytia
syncytia; cancer; cell adhesion;
                                                                                                                                                                                                                                                                                     Nucleotide sequence of a human endogenous retrovirus envelope protein.
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ilarity 91.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple sclerosis; rheumatoid polyarthritis; disseminated lupus erythematosus; pregnancy;
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           catcagccaacctccccaacagcacttgggttttcctgttgagagggggggactgagagac
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                                              gaaatctcagctgcacaacctctactacgccccaattcagcaggaagcagttagagcggt
                                                                                            ctggaccggcctgctagcccacgatctgatgttaatgacatcaaaggcacccctcctgag
                                                                                                                                                      caaattgttcttcaaatggagcaccagatggagtccatgactaagatccaccgtggaccc
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cgtcggccaacctccccaacagcacttaggttttcctgttgagatgggggactgagagac
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The present sequence represents an endogenetic retroviral nucleic acid fragment, which is associated with an autolimnune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimnune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoimnune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell proliferation in vitro.
                                                                                                                                                                                                               New nucleic acid from human endogenous retrovirus, useful e.g. diagnosis of autoimmune disease and complications of pregnancy contains at least part of the gag gene .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1038
                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                             Paranhos-Baccala G,
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pregnancy; multiple sclerosis; T cell proliferation;
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                      06-JUL-1998;
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Pred. No. 4.4e-152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis of autoimmune contains at least part c
                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid from human endogenous retrovirus, useful e.g. diagnosis of autoimmune disease and complications of pregnancy, contains at least part of the gag gene •
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                                 gaaatctcagctgcacaacctctactacgccccaattcagcaggaagcagttagagcggt
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(pos:790.792,aa:Phe)

(pos:793.795,aa:Thr)

(pos:812.814,aa:Leu)

(pos:818.820,aa:Ser)

(pos:865.867,aa:Gln)

(pos:1174.1176,aa:Arg)

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(pos:1174.1176,aa:Arg)

(pos:2017.2019,aa:Gln)

(pos:2017.2019,aa:Arg)

(pos:2044.2046,aa:Arg)

(pos:2089.2091,aa:Gln)

(pos:2089.2091,aa:Gln)
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Sequence

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Length 2782;

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CC on the basis of the PBS t-RNA motif used for the classification of human CC endogenous retrovirus (HERWs) the full length endogenous provirus which CC was been located on the long arm of human chromosome 7 (7921-22) has been CC designated HERV-W. The present invention describes proteins or peptides (I) having superantigen (SAg) activity comprising the ENV protein (ENV) CC of HERV-W, the surface protein (SU) and transmembrane (TM) sub-units. (I) cc have neuroprotective activity, and can be used in: vaccines; antisense-cc therapy; and HERV-W SAg activity inhibitors. (I) and encoding DNA/RNA are useful for diagnosing multiple sclerosis (MS) or HERV-W-associated CC disorders. (I) are also useful for identifying substances (and optionally crecovering) capable of binding to a retroviral superantigen associated CC with MS, substances capable of blocking stranscription or translation of HERV-W retroviral SAg is useful in therapy. Nucleic acid colored of SAg activity and being capable of preventing an immune response capable of blocking SAg activity, capable of binding to a retroviral Sag is useful in therapy. Nucleic acid completed with MS, or capable of binding to a retroviral CC capable of blocking SAg activity, capable of binding to a retroviral CC capable of blocking SAg activity, capable of binding to a retroviral CC capable of blocking SAg activity, capable of binding to a retroviral colored with MS, or capable of binding to a retroviral colored colored section of MS. (I) and nucleic acids encoding them are useful for CC diagnosing autoimmune disease. The present sequence encodes the CC diagnosing autoimmune disease. The present sequence encodes the CC diagnosing autoimmune disease. The present sequence encodes the CC diagnosing autoimmune disease.
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                                                                                                                                                           This sequence represents the complete sequence of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multip sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulin- dependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes associated with this susceptibility.
   6976
                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences from human endogenous retrovirus-Wexpressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnant
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proliferation;
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Search completed: June 20, 2002, 09:42:19 Job time: 8469 sec

AX001024 Sequence AF127229 Multiple AC019346 Homo sapi AC022171 Homo sapi AC010778 Homo sapi AL162912 Human DNA

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RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS,
ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID A
DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES
PATENT: WO 9002666-A 6 21-JAN-1999;
BIO MERIEUX (FR); OTT CATHERINB—(TR)
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Ounanian-Paraz, A., Sodoyer, M., Ott, C., Raj
Mallet, F., Mandrand, B. and Perron, H.
Molecular cloning and characterization of
associated with retrovirus-like particles
Virology 260 (1), 1-9 (1999)
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Pred. No. 3.3e-192;
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AC019346
Homo sapiens chromoso
SEQUENCE, 1 ordered p
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AC019346.4 GI:16418:
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                                                                                                                                                                                                                                                                                        Sequencing vector: Plasmid; n/a; 52% of reads
Sequencing vector: Plasmid; n/a; 68% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 176087 bases at least Q40
Consensus quality: 176095 bases at least Q30
Consensus quality: 176095 bases at least Q30
Insert size: 178000; agarose-fp
Insert size: 178000; agarose-fp
Quality coverage: 11.5 in Q20 bases; agarose-fp
Quality coverage: 11.7 in Q20.
* NOTE: This is a 'working draft' sequence. It currently
consists of I contigs: Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
fof the gaps between them are based on estimates that have
provided by the submittor.

* This sequence will be replaced
by the finished sequence as soon as it is swallable and
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1 (bases 1 to 176095)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Birren,B., Chromosome 18, clone RP11-497M7
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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-----Genome Center
Center: Whitehead Institute/ MIT Center for Genom
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t, A.F.A. & Green, P. (1996–1997)
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Center clone name: 497_M_7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
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/clone_lib="RPCI-11 Human
                          /clone="RP11-497M7"
                                                                           /chromosome="18"
                                                                                                   /db_xref="taxon:9606"
                                                                                                                           /organism="Homo sapiens"
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BASE COUNT
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                                                                                                                                                                                                                                                                              210336 bp
Homo sapiens chromosome 18 clone
SEQUENCE, 2 unordered pieces.
AC022171
                               Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Mao, J., Komp, C., Kottler, S., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Webb, C., Wilhelmy, J., Yu, S. and Davis, R.W.
Unpublished 2 (bases 1
                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 210336)
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                          AC022171.18 GI:13270574
HTG; HTGS_PHASE1; HTGS_DRAFT;
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                                                                                                                                                                                                                                            HTGS_FULLTOP;
                                                                                                                                                                                                                                                                                                                        RP11-407C18, WORKING
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JOURNAL
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Best Local Similarity
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                                                                  CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 58295
                                                                                          caaattgttcttcaaatggagcaccagatggagtccatgactaagatccaccgtggaccc 120
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Assembly program: Phrap; version 0.990319
Consensus quality: 208312 bases at least 040
Consensus quality: 208177 bases at least 030
Consensus quality: 209157 bases at least 030
Consensus quality: 209157 bases at least 030
Consensus quality: 209157 bases at least 020
Insert size: 199762; agarose-fp
Insert size: 210236; sum-of-contigs
Quality coverage: 8.7x in 020 bases; sum-of-contigs
Quality coverage: 8.7x in 020 bases; sum-of-contigs
NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morehouse, A.J., Oo
Yu, S. and Davis, R
Direct Submission
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Glukhov, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved.
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66569
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Sequencing Vector: plasmid; plasmid_accession;
Chemistry: Dye-primer; 10% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: hum-info@sequence.stanford.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:
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clone_end:T7"
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a 37228 c 37515 g 67816 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 66468: contig of 66468 bp in length 66568: gap of unknown length 9 210336: contig of 143768 bp in length Location/Qualifiers
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., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
.A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI human BAC library
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Pred. No. 1.2e-190;
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JOURNAL REFERENCE
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AUTHORS
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Submitted (22-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 30, 2000 this sequence version replaced gi:6087973. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Homo sapiens, clone RP11-2N15
                                                                                                                  Direct Submission
                                                                                                                                       Wyman,D., Ye,W.J., Zimmer,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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Primates;
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                                                                                                                                         Zody, M.
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http://ftp.genome.washington.edu/RM/RepeatMasker.html

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BASE COUNT
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Chemistry: Dye-terminator Big Dye; 1100% of
Assembly program: Phrap; version 0.960731
Consensus quality: 140899 bases at least (
Consensus quality: 144351 bases at least (
Consensus quality: 145949 bases at least (
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Insert size: 148024; sum-of-contigs
Quality coverage: 3.9 in Q20 bases;
Quality coverage: 4.8 in Q20 bases;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
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63442 98587: contig of 35146 bp in
98588 98687: gap of 100 bp
98688 148724: contig of 50037 bp in
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42007 63341: contig of 21335 bp
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/db_xref="taxon:9606"
/clone="RP11-2N15"
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2562: gap of 100 bp

7948: contig of 5386 bp in length

1048: gap of 100 bp

15800: contig of 7752 bp in length

15900: gap of 100 bp

25039: contig of 9159 bp in length

25039: contig of 9159 bp in length
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41906: contig of 16747 bp
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                                variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                            Submitted (22-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 8339)
                                                                                                                                                                                                                                                                                                               complete sequence. AL162912 AL121824 AL162912.1 GI:740
                                                                                                                                                                                                                                                                                                                                                               Human DNA sequence
                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                  Pearce, A.
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 AL162912
following abbreviations are used to associate primary accession bers given in the feature table with their source databases:
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Primates;
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gcatccacctctaaacatggggcttgcaacttagctcacacccgaccaatcagagagctc
                                                                                                                                                                                                                                                                                                               CATCAGCCAACTTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGTACTGAGAGAC
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                                                                                                                                   AGGACTAGCTGGATTTCCTAGGCCAACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACC 6023
                                                                                                                                                                                aggactagctggatttcctaggccaacgaagaatccctaagcctagctgggaaggtgact 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Group. Further information on the first sequence was finished as follows unless otherwise noted: all This sequence was finished as follows unless otherwise noted: all the first sequenced with an alternate of the first sequenced with an alternate sequence with a sequence with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sections only once, except for a Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. Rp6-198C4 is from the library Rp01-6 constructed by the group of Pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt IMPORTANT}: This sequence is not the entire insert of clone RP6-198C4 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           further details see
http://www.chori.org/bacpac/home.htm
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/db_xref="taxon:9606"
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94.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 579.2; DB 9; Pred. No. 4.4e-174;
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                                                                                               Direct Submission
Submitted (09-MAY 2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63
On Feb 16, 2001 this sequence version replaced 91:11597125.
                                                                                                                                                                                                                                               Waterston, R. H.
Direct Submission
Submitted (16-FEB-2001) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (27-JUN-2000) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; 1 (bases 1 to 136901) Sulston, J.E. and Waterston, R.
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Homo sapiens BAC clone RP11-95P9 from 7, complete sequence.
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Center project name: H_NH0095P09
                                    Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                         Center: Washington University Genome Center code: WUGSC
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clone sections once, between neighboring of This sequence may not represent the entire insert of this It may be shorter because we only sequence overlapping ections once, or longer because we provide a small overlap neighboring data submissions.

This sequence was all regions were o double finished as follows unless otherwise noted: double stranded, sequenced with an alternate

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chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:-8. The clone may be obtained either from libraries. Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute http://bacpac.med.buffalo.edu)

NEIGHBORING SEQUENCE INFORMATION:

рвасез.

The clone sequenced to the left is CTD-2023N18, 200 bp overlap; the clone sequenced to the right is CTA-250D13, 200 bp overlap. Actual start of this clone is at base position 127066 of CTD-2023N18; actual end is at base position 26937 of CTA-250D13.

base from There are polymorphic base differences stolen scolen data from a redundant clone RP11-636N5. The region from postition 29435 to 29729 consists of an insertion fragment RP11-636N5, which was originally found deleted RD11-2577 Location/Qualifiers

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FEATURES
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                                                                                                                                                                                 sequence.
AL583805.
AL583805.
requests: clonerequest@sanger.ac.uk
On Oct 2, 2001 this sequence version replaced gi:14702155.
During sequence assembly data is compared from overlapping cl.
Where differences are found these are annotated as variations
                                                Submitted (29-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                            Direct Submission
                                                                                           Clark
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Mammalia; |
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/rpt_family="AT_rich"
                                                                                                    ; Metazoa; Chordata; Eutheria; Primates; 1 to 89728)
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                                                                                                                              GAAATCTCAACTGCACAACAACTACTATGCCCCAATTCAGCAGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                 gaaatctcaactgcacaacccctactatgccccaattcagcgggaagcagttagagcggt
                                                                                                                                                                                                                      CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAACGACATTGAAGGCACCCCTCCTGAG
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                                                                                                                   TGTCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGCGGGGACTGAGAGAC
                                                                AGGACTAGCTGGATTTCCTAGGCGGAATAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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83730

83850

240

83610

83550

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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9

RP11-134K1 is from the library RPC1-11.1 constructed by the group of pleter de Jong. For further details see http://www.sanger.ac.uk/HGP/Chme.htm
                                                                                                                             al Similarity
598; Conserv
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This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RP11-134KI It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-134KI is at 89728 in this sequence. The true right end of clone RP11-60C15 is at 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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                                                                                                                             Conservative
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/clone_lib="RPCI-11.1"
17925 c 16432 g 25
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                      88.98;
                                                                                                                       Score 564.6;
Pred. No. 3.5e
0; Mismatches
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                                                                                                                          3.5e-169;
ches 34;
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RESULT 9
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FINITION
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AL451130 AC011776
AL451130.7 GI:18643757
                                                                                                                                                                                                                                       Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 40% of reads
Sequencing vector: plasmid; L08752; 40% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 206656 bases at least Q40
Consensus quality: 208766 bases at least Q30
Consensus quality: 210138 bases at least Q20
Insert size: 18186; 9.1% error; agarose-fp
Ouality coverage: 9.78x in Q20 bases; sum-of-contigs
Coverage: 12.66x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 10, 2002 this sequence version replaced gi:18151469. Draft Sequence Produced by Whitehead Institute/MIT Center for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clark, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: bA10G21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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     2460
2560
4644
4744
     4743: gap
6823:
                                   2559: gap
4643:
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2459: contig of 2459 bp in length
9: gap of 100 bp
4643: contig of 2084 bp in length
3: gap of 100 bp
6823: contig of 2080 bp in length
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Primates;
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Db 113775 CCCTGTATCTTTAACCTCCTTGTTAAGTGTGTCTCTTCCAGAATCGAAGCTGTAA---TA 113719
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Best Local Similarity
                                                                                                                                                          113538 TGTCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGCGGGGACTGAGAGAC
                                                                                                                                                                             361 gcatccacctctaaacatggggcttgcaaccttagctcacacccgaccaatcagagagctc 420
                                                                         gaaatctcaactgcacaacccctactatgccccaattcagcgggaagcagttagagcggt 240
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9153 9252: gap of 100 bp

9153 198727: contig of 189475 bp in length

198728 198827: gap of 100 bp

198828 202432: contig of 3605 bp in length

202433 202532: gap of 100 bp

202533 206117: contig of 3585 bp in length

206118 206217: gap of 100 bp

206218 205232: contig of 3315 bp in length

209533 209632: gap of 100 bp

209533 209632: gap of 2464 bp in length.
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2560. .4643
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/chromosome="9"
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38564 c 41164 g 68462 t
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198828. .202432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Earnhart.C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg.N., Ford.J., Foster,P., Frantz,P., Gablsi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karisson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,A., Luna,R., Ma,J., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Maner,G., Miner,Z., Mitchell,T., Mohabbat,K., Worgan,M., Morris,S., Musser,N., Nickerson,E., Nockenkwo,S., Oguh,M., Okwonu,G., Orgunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Ph.L.L., Quiles,M., Ren,Y., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
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                                                                                                                                                                                                                                                Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Walliamson, A., Wleczyk, R., Wooden, S., Worley, K., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Williamson, A., Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barbarla, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D. Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N. Buhay, C., Burcell, K. L., Byrd, N. C., Buhay, C., Burcell, K. L., Byrd, N. C., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, T. F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C. D., Cox, C., Coyle, M. D., Batharne, S. R., David, R., Davila, M. L., Davis, C., Coyle, M. D., Datharne, S. R., David, R., Delaney, K. R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H., Douthwalte, K. J., Draper, H., Dugan, Rocha, S., Durbin, K. J., Draper, R., Draper, H., Dugan, Rocha, R., Draper, R., Drap
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1 (bases 1 to 175040)

Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
     Unpublished 2 (bases 1
                                                                                                                                                         Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Weinstock,G. and Gibbs,R.
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                                                                                                       Direct Submission
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ccctgtatctttaacctccttgttaagtttgtctcttccagaatcaaaactgtaaaacta 60
                                                      CTGGACTGGCCTGCTAGCCCATGATCCGATGTTAATGACATCAAAGGCACCCCTCCCAAG
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93.8%;
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1; Gaps

1;

123189

Length 175040;

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Submitted (07-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 10, 2001 this sequence version replaced gi:9438656.
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
Contact: hgsc.help@bcm.tmc.edu
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/db_xref="taxon:9606"
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47210: gap of unknown length
80061: contig of 32851 bp in length
80161: gap of unknown length
112177: contig of 32016 bp in length
112277: gap of unknown length
112277: gap of unknown length
140321: contig of 28044 bp in length
140421: gap of unknown length
157447: contig of 17226 bp in length
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gap of unknown length
contig of 6496 bp in 1
Score 560.2; DB 2;
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LL56-APP region,
AP001538
AP001538.1 GI:73
                                                                                                                                                         Submitted (33-MAR 2000) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamhhara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                             1 (bases 1 to 174019)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 174,019 genomic DNA of 21q21.1-q21.2
Homo sapiens 174,019 genomic DNA of 2nq21.2
Published Only in DataBase (2000) In press
2 (bases 1 to 174019)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Similarity
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                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/clone="8838K11"
/map="21921.1-q21.2"
a 31416 c 32248 g 57052
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Homo sapiens genomic DNA, chromc AP001674 AL163219 BA000005
AP001674.1 GI:7768666
2 (bases 1 to 340000)
Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K., Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
                                                                                                                         and sequencing consortium Nature 405 (6784), 311-319
                                                                                                                                                              Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K., Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schillhabel,M. and Schudy,A. The DNA sequence of human chromosome 21. The chromosome 21 mapping
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patterson, D., Reichwald, K., Rump, A., Schillhabel, M., Schudy, A., Zimmermann, W., Rosenthal, A., Kudoh, J., Shibuya, K., Kawasaki, K., Asakawa, S., Shintani, A., Sasaki, T., Nagamine, K., Mitsuyama, S., Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordslek, G., Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordslek, G., Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordslek, G., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A., Reichelt, J., Kauer, G., Bloecker, H., Ramser, J., Beck, A., Klages, S., Hennig, S., Riesselmann, L., Dagand, E., Wehrmaeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * Institute of Molecular Biotechnology, Genome Analysis, Beutenbergstrasse 11, D-0745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de * URL: http://genome.imb-jena.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On May 30, 2000 this sequence version replaced gi:7717271.
The chromosome 21 mapping and sequencing consortium consisting
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
Sagamihara 228-8555, Japan,
* e.mail: hattorigsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
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On May 30,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * GBF, Dept. of Genome Analysis,
* Mascheroder Weg 1, D-38124 Braunschweig, Germany,
info.genome@gbf.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160-8582, Japan,
* e.mail: nshimizu@dmb-med.keio.ac.jp
* URL: http://www.dmb.med.keio.ac.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.mail: info-chr21@molgen.mpg.de
URL: http://chr21.rz-berlin.mpg.de/
L163219: Submitted (10-Apr-2000).
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93.7%;
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Pred. No. 1.7e-166;
0; Mismatches 39;
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27321 ACTAAATCTTGCAACTGCA 27303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel:81-42-778-9923, Fax:81-42-778-9924)
On Jul 14, 2000 this sequence version replaced gi:8117383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
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DRAFT SEQUENCE, 13 unordered
AP001545
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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Only in DataBase (2000) In press 2 (bases 1 to 149755)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 149755)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 149,755 genomic DNA of 18q21
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Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 145596 bases at least Q40
Consensus quality: 147102 bases at least Q30
Consensus quality: 147911 bases at least Q30
Consensus quality: 149711 bases at least Q30
Insert size: 148555; sum-of-contigs
Quality coverage: 10.98x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
------ Project Information
                                                                                                                                                                                                                                                                                                                             Center project name: HumDraft18
Center clone name: RP11-762G24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: RIKEN
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sapiens DNA, clone:RP11-762G24.
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NOTE: This is a 'working draft' sequence. It currently consider in this sequence record is arbitrary. Gaps between the control are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence are unknown. preserved NOTE: 144452 146768 148320 116306 123885 130456 133720 137517 44929 82703 101445 141641 44828 contig of 82602 contig of 101344 contig of 116205 contig of 123784 contig of 133619 contig of 137416 contig of 141540 contig of 144551 contig of 146667 contig of 148219 c S a 'working draft' 44828 37674 18642 14761 7479 6477 3164 3164 3697 4024 2711 2216 10 10 10 10 in length Length

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BASE COUNT
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    Conservative
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133720. .137416
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101445. .116205
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/db_xref="taxon:9606"
/chromosome="18"
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31173 c 31787 g 42682
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146768. .148219
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148320. .149755
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144452. .146667
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130456. .133619
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123885. .130355
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130355: cont
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149755: cont
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                                          86.9%;
91.8%;
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Score 551.8; DB 2;
Pred. No. 4.9e-165;
0; Mismatches 52;
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                                                                                    Length 149755;
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JOURNAL REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aggactagctggatttcctaggccaacgaagaatccctaagcctagctgggaaggtgact 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAACTGCAAAAAATAAAAATAAAAAAATTAAAAA 67701
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boyuslavki, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Johnson, R., Landers, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacGonald, P., McCarthy, M., McEwan, P., McKernan, K., McCPath, M., McCPath, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome 18 clone SEQUENCE, 3 unordered pieces. ACQ90313
                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates;
1 (bases 1 to 152775)
Birren,B., Linton,L., Nusbaum,
                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                 Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 18, clone RP11-762G24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC090313.2 GI:14971265
HTG; HTGS_PHASE1; HTGS_
                                                                                                                                                                                                                                                                                                              (bases 1 to 152775)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA linear
RP11-762G24 map 18,
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WORKING DRAFT
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BASE COUNT
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O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Sougnez, C., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Trigvillo, J., Vassiliev, H., Viel, R., Vo, A.,
Willess, P., R., Vo, A.,
Willess, P., Wassiliev, H., Viel, R., Vo, A.,
Wassiliev, H., Wassiliev, H., Vo, A.,
Willess, P., Wassiliev, H., Vo, A.,
Wassiliev, H., Wassili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 20, 2001 this sequence version replaced gi:12957949. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zembek,L., Zimmer,A. and Zody,M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator Big Dye; 100% of read: Assembly program: Phrap; version 0.960731
Consensus quality: 151319 bases at least 040
Consensus quality: 152154 bases at least 030
Consensus quality: 152385 bases at least 020
Insert size: 146000; agarose-fp
Insert size: 152575; sum-of-contigs
Quality coverage: 8.0 in 020 bases; agarose-fp
Ouality coverage: 7.6 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L12582
Center clone name: 762_G_24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149090 149189: gap of 100 l
149190 152775: contig of 3586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
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Query Match

98

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Score

551.8;

DB 2;

Length 152775;

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                                                                                                                                                                                                                                                                                              163803 bp
Homo sapiens chromosome 5 clone
AC093531
AC093531.2 GI:16945981
Submitted (16-NOY-2001) DOE Joint Genome Institute, Drive, Walnut Creek, CA 94598, USA
                                                             Submitted (31-AUG-2001) Production Sequencing Genome Institute, 2800 Mitchell Drive, Walnut 3 (bases 1 to 163803)
                                                                                                                                                                                          Mammalia; Eutheria; Pr
1 (bases 1 to 163803)
DOE Joint Genome Insti
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Mammalia; Eutheria; Primates;
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Best Local Similarity 93.2%;
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Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
Location/Qualifiers
1. 163803
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Finishing Completed at Stanford Human Genome Center
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Sequence Produced by DOE Joint Genome Institute
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a 31372 c 29086 g 48548 t
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Search completed: June 20, Job time: 10754 sec

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BE019603 ba84f03.y
BG572445 602593490
AA776439 Zj50h06.s
AL601847 DKF2p313K
AQ776289 HS_5528.A
R68740 y114906.r1
AQ725469 HS_5403.A
BG004254 RC6-GN028
B1052569 RC5-GN028
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1 (bases 1 to 723)

Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                 AU138405
AU138405.1
                                                                                       Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
                                                                                                                                                                                       HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                      Homo sapiens
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                   210
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PLACE1 Homo sapiens
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BIO55427
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BIO53220
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                  : pME18SFL3"
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BI056079 RC5-GN028
BI05320 PM0-GN021
BI05320 PM0-GN021
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Euteleostomi;

BI056593

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CITBI-E1-2506C15.
DNA sequence.
AQ261133
AQ261133.1 GI:37
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679; Conserv
                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 631)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,I
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
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        Use of a random human
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CONTact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Ge
                                                                                                                                                                                                                                                                                                                  TCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTTAGCAATACTATAGACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: M13-21 Class: BAC ends.
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AU138097 PLACE1
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Hel
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo,
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,)
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S.
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Tissue Procurement: ATCC
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                                      194
                    /tissue_type="choriocarcinoma"
/lab_host="pHIOB (phage resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Birectionally cloned into EcoRI/XhoI sites using the place to the place of the place
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Query Match
Best Local Similarity
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1 (bases 1 to 586)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                       BE019503 586 bp mRNA linear EST 06-JUN-2000 ba84f03:y1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2907101 5' similar to TR:095244 ENVELOPE PROTEIN ;contains Alu repetitive element; mRNA sequence.
                                          Contact: Robert Strausberg, Ph
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                      Unpublished (1999)
Contact: Robert St
                                                                                                                                                                     Homo sapiens
cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing
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Seq primer: -40RP from Gibco
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/db_xref="taxm:3606"
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH20B (phage-resistant)
/lab_host="DH20B (phage-resistant)"
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   TACAAACTATCTCAAGAACTAAATGGGGACATGGAACGGGTCGCCGACTCCCTGGTCACC
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
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National Institutes of Health, Mammalian
Unpublished (1999)
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/lab_host="PDH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
/note="Organ: placenta; Vector: pDNR-LIB (ggccattatggcc);
/note="Organ: placenta; Vector: pDNR-LIB (clontech);
/note="Organ: placenta; Vector: pDNR
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/db_xref="taxon:9606"
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1 (bases 1 to 427)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.

WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2350h06.sl Soares_fetal_liver_spleen_lnFLS_Sl Homo clone IMAGE:453755 3' similar to SW:ENV_SMRVH p214. POLYPROTEIN PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 410.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University Scho
4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
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                    /lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
/with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library. 1st strand cDNA was primed
double-stranded cDNA was ligated
                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:1390111"
/db_xref="taxon:9606"
/clone="IMAGE:453755"
                                                                                                                                                                              /dev_stage="20 week-post conception fetus"
                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                      clone_lib="Soares_fetal_liver_spleen_1NFLS
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Eco RI adaptors
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                          Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Can. Research Center (DKFZ); Email s. Wiemannedkfz- heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cD. sequencing consortium of the German Genome Project. No sl seguences.
                                                                                                                                                                                                                                                                                                                                    AL601847 718 bp mRNA linear EST 14-AL DKFZp313K157_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone DKFZp313K157 5', mRNA sequence.
AL601847
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                                                                                                                                     Contact: Ottenwaelder B
                                                                                                                                                    Unpublished (2001)
                                                                                                                                                                                                             Ottenwaelder, B.,
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clone (DKFZp313K157) is
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Proc. Nat 99380589
                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 586)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a
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AQ776289

HS_5528_A2_B10_T7A RPCI-11 Human Male BAC Library Homo genomic clone Plate=1104 Col=20 Row=C, DNA sequence.

AQ776289

AQ776289.1 GI:5656017

GSS.
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          Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                             Homo sapiens
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/ob_xref="taxon:9606"
/clone="DkFZg313K157"
/clone_lib="313 (synonym: h)
/dev_stage="adult"
/lab_host="DHIOB"
/note="vector: pTriplEx2; s:
cDNA-collection"
132 c 156 g 209 t
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GERMANY; Email: clone@rzpd.de.
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                     agatcaacttaactccctagcagcagtagtccttcaaaatcgaagagctttagacttgct
                                                                                               actatctcaagaaataaatggtgacatggaacaggtcactgactccctggtcaccttgca 1106
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  AGATCAACTTAACTCCCTAGCAACAGTAGTCAATCACNATCGAAGAGCTTTAGACTTGCT
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401 Queen Anne Avenue North, Searel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.htsc.washington.edu
Plate: 1104 row: C column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm or from Resear h Genetics (info@resgen.com). BAC end Web Server:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="Plate=1104 Col=20 Row=C"
/clone_lib="RPCI-11 Human Male BAC Library"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Source: IMAGE Consortium, LLNL Source: IMAGE Consortium, LLNL free through LLNL; contact the This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1644 Std Error: 0.00
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holma,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons, Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterst,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1995)
Contact: Wilson RK
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Location/Qualifiers
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Insert Size: 1644
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="GDB:545824"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares placenta Nb2HP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:139258"
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                                                                                                                                                        24.1%;
91.3%;
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                                                                                                                                      Score 356.4; DB 1
Pred. No. 4.5e-84;
0; Mismatches 36
                                                                                                                                                                         DB 10;
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                                                                                                                                           Fax: (206) 616-388/
Email: ]wallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 979 row: I column: 3
Seq primer: T7
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 608)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ725469 608 bp DNA linear GSS HS_5403_A1_E02_T7A RPCI-11 Human Male BAC Library Homo genomic clone Plate=979 Col=3 Row=I, DNA sequence.
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Location/Qualifiers
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AQ725469
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/note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECOR.
Male blood DNA was isolated from one randomly chosen
and partially digested with a combination of ECORI ar
                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=979 Col=3 Row=I"
/clone_lib="RPCI-11 Human Male
/sex="male"
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g,J., Zhao,S.,
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Adams,M.D.
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1 (bases 1 to 411)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jonganeel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                 Tel: +55-11-2704922
Fax: +55-11-2707001
                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 an
                                                                                                               Contact: Simpson A.J.G.
                                                                                                                                 20202663
                                                                                                                                                                sequence tags
                                                                                                                                                                              Shotgun sequencing
                                                                                                                                                                                                 Simpson, A.J.
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asimpson@ludwig
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Souza, S.J. and

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                                                                                                                                                                                                                                                                                                                                            agcagctctaatattgttactcctctttggac 1396
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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RC5-GN0282-220101-011-G04
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/db_xref="taxon:9606"
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Pred. No. 9.3e-84;
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                                                                                                           tcccacacgaatagtctgcc 790
                                                                                                                                                                                                                                                 cgttttagtaggacctcttgtttccaatctggaaataacccatacctcaaacctcacctg
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC5&t2=RC5-GN0282-
220101-011-G04&t3=2001-01-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 381.
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Tel: +55-11-2704922
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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   BI056595
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/db_xref="taxon:9606"
/clone_lib="GN0282"
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Pred. No. 2.8e-82;
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gtaggacctcttgtttccaatctggaaataacccatacctcaaacctcacctgtgtaaaa
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                                                                                                  atccctgttcctgaacaatggaacaacttcagcacagaaataaacaccacttccgtttta
                                                                                                                                                                                 gcccmaaaccctactaactgttggatgtgcctccccctgcacttcaggccatacatttca
                                                                               GCCCAAAACCCTACTAACTGTTGGATATGCCTCCCCCTGAACTTCAGGCCATATGTTTCA
                                                                                                                                                                                                                                                 ACCCATACTCGCCTGGTAAGCCTATTTAATACCACCCTCACTGGGCTCCATGAGGTCTCG
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1 (bases 1 to 376)

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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This sequence was derived from the FAPESD/LICR Human
Those tribine and the following URL
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
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Location/Qualifiers
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210201-013-G04&t3=2001-02-21&t4=1)
Seq.primer: puc 18 forward
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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//db_xref="taxon:9606"
//clone_lib="GN0282"
//dev_stage="Adult"
//notc="Organ: placenta_normal; Vector: pucl8; Site_1: Smal
/ notc="Organ: placenta_normal; Vector: pucl8; Site_1: Smal
/ notc="Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-GN0282-
220101-011-A04&t3=2001-01-22&t4-1)
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1 (bases 1 to 373)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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                                                                                                                                                                                               /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI; A mini-library was made by Cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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199 111	ESULT 1 Sequence 3, Application patent No. 6312921 GENERAL INFORMATION: APPLICANT: Jacobs, Ker APPLICANT: LaVallie, IAPPLICANT: Evans, Chen APPLICANT: Evans, Chen APPLICANT: Evans, Chen APPLICANT: Metherg, Da APPLICANT: Metherg, Man APPLICANT: Metherg, Man APPLICANT: Metherg, Man APPLICANT: Mi, Sha APPLICANT: Genetics If TILE REFERENCE: 6006B CURRENT APPLICATION NUCURRENT PILING DATE: 1 NUMBER OF SEQ ID NOS: SOFTWARE: Patentin Venum Seq ID No Sep ID NO GRANISM: Homo Sapier Opery Match Best Local Similarity Query Match Best Local Similarity	44 55 55 55 55 55 55 55 55 55 55 55 55 5
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NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 876-5891
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 542 base pairs
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 184; Conserv
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APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PI
TITLE OF INVENTION: ENCODING TI
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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STRANDEDNESS:
TOPOLOGY: lin
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STREET: 8:
CITY: Camb
CITY: Mas
STATE: Mas
COUNTRY: U
ZIP: 0214
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87 CambridgePark Drive
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LaVallie, Edward
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Treacy, Maurice
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US-08-721-489-2
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Best Local Similarity
                                                                                                                                                                                                                                    Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT:
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NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
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                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
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CLASSIFICATION: 530
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CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 542 base pairs
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Treacy, Maurice
Spaulding, Vikki
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Pred. No. 1.4e-46;
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0. 6001987
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563C
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & B
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1240 gtcactgagaaagttaaagaaattcgagatcgaatacaatgtagagcagaggagcttcaa 1299
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                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                  GGAGGACTCTGCACCTTCTTAGGGGAAGAGTGTTGTTTTACACTAACCAGTCAGGGATA
                                                      gggggaacctgtttattttaggagaagaacgctgttattatgttaatccaatccagaatt 1239
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Frederic BEDIN
Glaucia PARANHOS-BACCALA
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Pred. No. 4.1e-37;
0; Mismatches 234;
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US-08-691-563C-46
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                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1859 base pairs
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REFERENCE/DOCKET NUMBER: WPB 38588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
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1036 ttctactacaaactatctcaagaaataaatggtgacatggaacaggtcactgactccctg 1095
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FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: BETTINGER, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Oliff & Berridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR TITLE OF INVENTION: THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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APPLICANT: Frederic BESSME
APPLICANT: Frederic BEDIN
APPLICANT: Glaucia PARANHOS
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22314
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                                                          Local
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TELEPHONE: 703-836-2787
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                                       11 Similarity
257; Conserv
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                                         Conservative
                                                                                                                                                                                    single
                                                      8.9%;
                                     Score 131.2; I
Pred. No. 2e-3:
0; Mismatches
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                                                          2e-32
                                                                       DB 3;
                                       183;
                                                                       Length 1859;
                                       Indels
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                                     Gaps
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                                                      TELEX: 248345
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pair
                                                                                                            REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERALD M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WITTER, RICHARD L.
APPLICANT: YANAGIDA, NOBORU
TITLE OF INVENTION: VACCINE COMPRISING FOWLPOX VIRUS
TITLE OF INVENTION: RECOMBINARYS EXPRESSING THE ENVELOPE GLYCOPROTEIN OF
TITLE OF INVENTION: AVIAN RETICULOENDOTHELIOSIS RETROVIRUS
NUMBER OF SEQUENCES: 2
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                                                                                        TELEPHONE: 703-205-8050
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FILING DATE: 19930121
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WITTER, RICHARD L.
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   Query Match
Best Local S
Matches 263
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APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
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Best Local Similarity
Matches 268; Conserv
                                                                                                                                                SOFTWARE: PatentIn SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09078294 Patent No. 6265211
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
                                                                                                                                                                               NUMBER OF SEQ ID NOS: 29
                                                                                                                LENGTH: 80246
TYPE: DNA
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HYPOTHETICAL: NO
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                    Similarity
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Pred. No. 9.2e-28;
0; Mismatches 252;
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Score 114.8; D
Pred. No. 3.8e-
0; Mismatches
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                                                      Query Match
Best Local Similarity 55.0
Conservative
                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. SEQ ID NO 1
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APPLICANT: Collins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09011745 Patent No. 6165715
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
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EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
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                       aaactatctcaagaaataaatggtgacatggaacaggtcactgactccctggtcaccttg 1104
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                                                                   7.7%; Score 114.2; DB 4; 55.0%; Pred. No. 8e-27; ative 0; Mismatches 183;
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APPLICANT: Welss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
ROBERLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
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US-09-011-745-8
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Patent No. 6165715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 8
LENGTH: 5865
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                                                                                                                                                                                                                                                                       LOCATION: (3612)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (3612)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
NAME/KEY: misc_feature LOCATION: (3800)
                                         FEATURE:
                                                    OTHER INFORMATION: n is
                                                                     NAME/KEY: misc_feature LOCATION: (3799)
                                                                                                             FEATURE:
                                                                                                                          OTHER INFORMATION: n is
                                                                                                                                             NAME/KEY: misc_feature LOCATION: (3614)
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LOCATION: (3611)
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; LENGTH: 80595
; TYPE: DNA
; ORGANISM: Nucleotide sequence
US-09-078-294-3
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; OTHER INFORMATION: n is
US-09-011-745-8
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                                                               Query Match
Best Local S
Matches 206
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Patent No. 6265211
GENERAL INFORMATION:
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Best Local Similarity
Matches 224; Conserv
                                                                                                                                                                                                                          APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION: n is
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                                                               Local Similarity 57.5
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tggcagcagtgactctccaaaaccgctgaggcctagactctcatgttgagaaaggaag--
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Pred. No. 1.3e-26;
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APPLICANT: COllins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09011745 Patent No. 6165715
                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (3913)
OTHER INFORMATION: n is any
-09-011-745-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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TYPE: DNA
                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (3912)
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LOCATION: (3911)
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les 224; Conserv
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                                                     Score 70; DB 4; Le
Pred. No. 2.4e-12;
0; Mismatches 215;
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                                                                                       Length 3925;
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APPLICANT: COLLINS, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Francois Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application Patent No. 6165715
                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEO ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
         PEATURE: misc_feature LOCATION: (3777)
                                                                NAME/KEY: misc_feature
LOCATION: (3776)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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LOCATION: (3774)
OTHER INFORMATION: n is
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
OTHER INFORMATION: n is
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; LOCATION: (3965)
; OTHER INFORMATION: n is
US-09-011-745-5
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Best Local Similarity
Matches 217; Conserv
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                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Jay A.
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NAME/KEY: misc_feature
TOATTON: (3962)
TOATTON: n 1
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NAME/KEY: misc_feature
LOCATION: (3963)
OTHER INFORMATION: n is
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TITLE OF INVENTION: MOLECULAR SEQUENCE OF
TITLE OF INVENTION: AND METHODS OF USE
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                                                                                   NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
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COMPUTER
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             COUNTRY: USA
ZIP: 02109-1875
                                           STATE:
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Pred. No. le-11;
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Best Local Similarity
Matches 144; Conserv.
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                                    FILING DATE:
CLASSIFICATION:
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RESULT 14
US-08-716-351A-5
; Sequence 5, Application
; Patent No. 6033905
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-766-528-1
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TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,351A
                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1763 CGAAGGGAAAAGGAAACTACTCAAGGGTGG 1792
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ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MG
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: PCT, FILING DATE: 06-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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14-DEC-1995
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Gaps

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ATTORNEY/AGENT INFORMATION:

'AGENT IN.
Bastian, Kevin L.
Bastian, Kevin L.
15

REFERENCE/DOCKET NUMBER: REGISTRATION NUMBER:

15280-128-1PC

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Best Local Similarity 56.1
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 543-504.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    6919
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                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
                                             APPLICATION NUMBER: US/0
FILING DATE: 10-UUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                         OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1087 gactccctggtcaccttgcaagatcaacttaactccctagcagcagtagtccttcaaaat 1146
FILING DAIL.

ATTORNEY/AGENT INFORMATION:
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CITY: F
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LOCATION: 1..10970
OTHER INFORMATION: /standard_name=
OTHER INFORMATION: vector"
                                                                                                                                                                         COMPUTER:
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Z: DNA (genomic)
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Pred. No. 1.9e-11;
0; Mismatches 100
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Best Local Similarity
Matches 227; Conserv
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INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
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                                                                                                                                AATAGATCCCCCTGGTTTACCACCTTAATCTCCACCATCATGGGACCTCTAATAGTACTC 1776
                                                                                  atattgttactcctctttggaccctgtatctttaacctccttgttaagtttgtctcttcc 1434
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Pred. No. 1.5e-11;
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Search completed: Job time: 8391 sec June 20, 2002, 09:38:01

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Database
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Maximum DB seq
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Perfect score:
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Listing first 45 summaries
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2 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT: *
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4 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT: *
5 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT: *
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6 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT: *
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Com
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Clone C15 from MSR
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	Complete human end HERV-W envelope pr Human endogenous r 5' non coding, 3' Human breast cell Human foetal liver Probe #4444 for ge Human brain expres Human bone marrow Probe #4541 for ge Probe #4566 used t Probe #4413 used t Probe #4413 used t Human endogenous r

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ALIGNMENTS

RESULT AAV43217 Multiple sclerosis associated retrovirus; MSRV; MS; gag gene; env gene; rheumatoid arthritis-associated AAV43217; (INMR) BIO MERIEUX. 26-NOV-1997; 04-JUN-1998. W09823755-A1 Multiple sclerosis associated retrovirus Multiple sclerosis associated retrovirus fragment 5 29-DEC-1998 (first entry) AAV43217 standard; cDNA; 1481 BP 26-NOV-1996; 96US-0756429 97WO-IB01482 Location/Qualifiers arthritis-associated virus; ss

Human endogenous

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Best Loc
Matches
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ВP

DE Nucleotide sequence of the MSRV-1 3' env and LTR regions

entry)

MSRV-1; pol region; long terminal repeat; LTR; RU5 region; retrovirus; ss.

OS Multiple Sclerosis retrovirus 1.

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                                                                                              The present sequence encodes an envelope protein of MSRV-1. The envelope protein expressed by the endogenous human retrovirus MRSV-1 has superantigen activity associated with autoimmune disease. The protien can be detected using the method of the invention. The specification describes a process for detecting activity of a superantigen in a biological sample. The process comprises identifying large scale expansion or loss of lymphocytes that carry at least one of the Vbetal6 and/or Vbetal7 determinants. The method is used to screen for agents that inhibit the superantigen, especially those associated with MRSV-1 which is implicated in autoimmune disease, particularly multiple sclerosis. These agents are potentially useful for treatment or prevention (e.g. as vaccines) of autoimmune diseases.
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Query Match Best Local Matches 1390;

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treating, preventing or ameliorating medical conditions in humans and animals. Detection of the levels of the proteins can be used for the diagnosis of e.g. pre-eclampsia, placental pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested activities include nutritional activity (e.g. in feeds), cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemastapolesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemastatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cacherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotide sequences are also stated to be useful for gene therapy.
                                                                                                                                                                                                                                                     This is the human secreted protein AJ172_2 nucleotide sequence, obtained from a human adult testes cDNA library. The invention relates to secreted human and murine proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for
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New human retrovirus HERV-W ENV proteins/peptides having superantigen activity useful for diagnosing and treating multiple sclerosis -

Claim 13; Fig 10; 94pp; English.

On the basis of the PBS t-RNA motif used for the classification of human CC endogenous retrovirus (HERW9) the full length endogenous provirus which CC was been located on the long arm of human chromosome 7 (7921-22) has been CC designated HERV-W. The present invention describes proteins or peptides (I) having superantigen (SAg) activity comprising the ENV protein (ENV) CC of HERV-W, the surface protein (SU) and transmembrane (TM) sub-units. (I) CC have neuroprotective activity, and can be used in: vaccines; antisense-CC useful for diagnosing multiple Sclerosis (MS) or HERV-W-associated CC disorders. (I) are also useful for identifying substances (and optionally recovering) capable of binding to a retroviral superantigen associated CC with MS, substances capable of blocking transcription or translation of HERV-W retroviral SQG is useful of SAg activity and being sagactivity and substances CC devoid of SAg activity and being capable of superantigen. A protein or peptide derived from (I), modified to be CC devoid of SAg activity and being capable of subrances caid CC molecules encoding (I) are useful as vaccines against MS. Substances CC capable of blocking SAg activity, capable of binding to a retroviral CC userantigen associated with MS, or capable of binding to a retroviral CC capable of blocking SAg activity, capable of binding to a retroviral CC userantigen associated with MS, or capable of binding to a retroviral CC capable of SAG (I) and nucleic acids encoding them are useful for CC diagnosing autoimmune disease. The present sequence encodes the CC diagnosing autoimmune disease. The present sequence encodes the

Sequence 1617 B₽; 442 Α, 452 Ç 296 ç; 427 Η, 0 other;

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The present sequence encodes a human endogenous retrovirus envelope protein. The specification describes a method for detecting expression of an envelope protein from a human endogenous retrovirus (HERV), in cells, of a tissue or culture. The method comprises detecting syncytia formation due to the fusogenic properties of the envelope protein. Envelope polypeptides and polynucleotides are used to produce therapeutic or prophylactic compositions, particularly for treatment of cancer, to correct defects in placental development (or other natural formation of other types of syncytia), and to promote adhesion of cells

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Disclosure;

Page

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                       On the basis of the PBS t-RNA motif used for the classification of human endogenous retrovirus (HERVs) the full length endogenous provirus which was been located on the long arm of human chromosome 7 (7q21-22) has been designated HERV-W. The present invention describes proteins or peptides
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(pos:790...792,aa:Phe)
(pos:793...795,aa:Thr)
(pos:812...814,aa:Leu)
(pos:818...820,aa:Ser)
(pos:865...864,aa:Tyr)
(pos:865...867,aa:Gln)
(pos:1174...1176,aa:Arg)
(pos:1174...1176,aa:Arg)
(pos:2017...2019,aa:Lys)
(pos:2026...2028,aa:Arg)
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CC of HERV-W, the surface protein (SU) and transmembrane (TM) sub-units. (I) have neuroprotective activity, and can be used in: vaccines; antisense-cc therapy; and HERV-W ASQ activity-inhibitors. (I) and encoding DNA/RNA are useful for diagnosing multiple scherosis (MS) or HERV-W-associated CC disorders. (I) are also useful for identifying substances (and optionally recovering) capable of binding to a retroviral superantigen associated CC with MS, substances capable of blocking SAg activity and substances (compable of blocking transcription or translation of HERV-W retroviral CC superantigen. A protein or peptide derived from (I), modified to be CC devoid of SAg activity and being capable of generating an immune response CC against HERV-W retroviral SAg is useful in therapy. Nucleic acid CC molecules encoding (I) are useful as vaccines against MS. Substances CC capable of blocking SAg activity, capable of binding to a retroviral superantigen associated with MS, or capable of binding to a retroviral constantigen associated with MS, or capable of blocking transcription or CC preventing MS, obtained using (I) are useful for the treatment and CC preventing MS, obtained using (I) are useful for the treatment and CC preventing autoimune disease. The present sequence encodes the Specifically claimed envelope protein of HERV-W designated G.
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Sequence 2782 BP; 741 A 768 Ç 564 G; 709 Ŧ; 0 other;

Best Local Similarity Matches 1373; Conser

Conservative

0;

108; DB 22;

Gaps

0

Length

2782; 0

Score 1308.2; Pred. No. 0; 0; Mismatches

88.3%; 92.7%;

Match

δÃ 밁 Qy B ρ В Q ₽ ρ Вb Qy Вb Ş 밁 δÃ Вþ 20 밁 Qy 밁 8 Ş 멍 1183 1363 1303 1123 1003 1243 1063 481 421 361 301 241 943 181 883 823 661 121 763 61 هسر atggccctcccttatcatacttttctctttactgttctctttaccccctttcgctctcact 60 acgcggcttcctggaaatattgatgccccatcatataggagtttatctaagggaaactcc ggacctcttgtttccaatctggaaataacccatacctcaaacctcacctgtgtaaaattt cctgttcctgaacaatggaacaacttcagcacagaaataaacaccacttccgttttagta caaaaccctactaactgttggatgtgcctccccctgcacttcaggccatacatttcaatc catactcgcctggtgagcctatttaataccaccctcactcggctccatgaggtctcagcc ggcacctctagcccctacaaaggactagatctctcaaaactacatgaaaccctccgtacc agcacccctagcccctacaaaggactagttctctctaaaactacatgaaaccctccgtacc ggagtcactgtctgttggacttacttcacccaaactggtatgtctgatgggggtggagtt ggagccactgtctgttggacttacttcacccataccagtatgtctgatgggggtggaatt catgcaaatactcattattggacaggaaaaatgattaatcctagttgtcctggaggactt catgcaaatactcattattggacagggaaaatgattaatcctagttgtcctggaggactt accttcactgcccacacccatatgccccgcaactgctatcactctgccactctttgcatg accttcactgcccacacccatatgccccgcaactgctataactctgccactctttgcatg atgcagcgtcccggaaatattgatgccccatcgtataggagtctttctaagggaaccccc gcacccctccatgccgctgtatgaccagtagctcccctcacccagagtttctatggaga gcaccccctccatgctgctgtacaaccagtagctccccttaccaagagtttctatgaaga atggccctcccttatcatatttttctctgtagtgttctttcaccctgtttcactctcact 822 cctgtacctgaacaatggaacaacttcagcacagaaataaacaccacttccgttttagta caaaaccctactaactgttggatatgcctccccctgaacttcaggccatatgtttcaatc catactcgcctggtaagcctatttaataccaccctcactgggctccatgaggtctcggcc 1122 300 882 660 1362 600 540 1242 480 1182 360 1062 1002 240 942 180

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Query Match
Best Local S
Matches 1372
                                                                                                                                                                               This sequence represents clone cl.PH74 of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulindependent diabetes and related pathologies) and of abhormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes
                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                 Sequence
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Matches 1372; Conser
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Local Similarity nes 1218; Conser

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Mismatches

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The invention relates to a spatially-addressable set of single exon cc nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting ct the probes with a collection of detectably labelled nucleic acids cound to each probe of the microarray. The probes are useful for cc verifying the expression of regions of genomic DNA predicted to cc encode proteins. They are useful for gene discovery, and for cc determining predisposition and/or prognosing breast disease. Gene cc expression analysis is useful for assessing the toxicity of chemical cc agents on cells. The microarray of this invention presents a far greater cd inversity of probes for measuring gene expression, with far less bias concept approduction of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Cc Note: The sequence data for this pattent did not form part of the cromator of the security of probes is a single exon nucleic acid probe of the invention. The content of the sequence data for this pattent did not form part of the content of the microarray of this pattent did not form part of the content of the content of the sequence of the invention.
Query Match
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                             ctggaccctggggcctcctcagccaatggatgccctggattctccccttcttaggacctc
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published not not compared directly
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27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
30-JUN-2000;
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REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM RESULT 1
AX001027
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DEFINITION
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1 (bases 1 to 1481)

Ott,C. and Bedin,F.

RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICU ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, PATENTIC WOODSTIC, PROPHYLACTIC AND THERAPEUTIC USES
PATENT: WO 9902666-A 9 21-JAN-1999;
BIO MERIEUX (FR); OTT CATHERINE (FR)
LOCATION/Qualifiers AX001027 1481 bp Sequence 9 from Patent WO9902666. AX001027 unidentified unidentified AX001027.1 GI:7241264 412 a /organism="unidentified" /db_xref="taxon:32644" 410 c 261 g 39 1. .1481 398 DNA linear PAT 10-MAR-2000 IN PARTICULAR

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Multiple sclerosis assocenv-like mRNA sequence.
AF127228
AF127228.1 GI:5726293
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                                                                                                                                    Direct Submission
Submitted (10-FEB-1999) UMR103 CNRS, biomerieux,
D'Italie, Lyon 69007, France
Docation/Qualifiers
1, 1932
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/db_xref="taxon:89382"
/clone="CLI5"
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/note="similar to env but i codon; includes signal pept TM regions"
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/note="in clones CLI5-2 and
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RESULT 3
AL390039/c
LOCUS
DEFINITION

AL390039 162579 bp DNA linear PRI 22-DEC-2000 Human DNA sequence from clone RP13-383K5 on chromosome Xq22.1-24 Contains ESTs, STSs and GSSs. Contains a novel gene and a novel gene similar to NUP62 (nucleoporin 62kD), complete sequence.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

> gene similar AL390039 AL390039.10 HTG; nucleopc

0039.10 GI:10186780 nucleoporin; NUP62.

Homo sapiens

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 162579)
Grafham, D.
Direct Submission
Submitted (19-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

requests: clonerequest@sanger.ac.uk

On Sep 19, 2000 this sequence version replaced gi:9944073.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //www.chori.org/bacpac/home.htm
                                                                                                                                           /note="AluSx repeat: 8420. .8487
                                                                                                                                                                                         /note="L1M4 repeat: 8099. .8419
                                                                                                                                                                                                                                                                                      /note="L1M4 repeat: matches 2857. .3036 of consensus" 6751. .7063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5152
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSq repeat: matches 1. .313 of consensus"
5917. .6014
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/note="7HE1B repeat: matches 1.
10519. .10807
/note="Alusq repeat: matches 3.
11343. .11416
                                                                                            /note="L1MC/D repeat: matches 10039. .10396
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1457. .2938
/note="LIMEc repeat: matches 356. .1897 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                      note="49 copies 2 mer ga 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note-"L1PA15 repeat: matches 5325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note-"L1MA8 repeat: matches 6120.
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/note="L2 repeat: matches 2213.
complement(19352. .19843)
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                                                                                                                                                                                                                                 /note="HERV17 repeat: 22298. .22742
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18812. .19057
/note="AluSx repeat: matches 1.
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18706. .18811
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18213. .18318
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/note="L2 repeat: matches 2688.
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23049 .23286
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14255. .14807
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13519. .13853
| note="MER7A repeat: matches 1. .346 of consensus"
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15885. .16086
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/note="FLAM_C repeat: matches 2. .124 of consensus"
13228. .13518
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                  Ll repeat: matches 3097. .4043 of consensus".24593
                                                   L1M4 repeat: matches 4019. .4084 of consensus" .24305
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repeat: matches 1.
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                                  CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA
                                         cctgttcctgaacaatggaacaacttcagcacagaaataaacaccacttccgttttagta
                                                                   CAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCAGGCCATACATTTCAATC
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26981. .27154
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/note="L1M3 repeat:
25437. .25742
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Homo sapiens
Eukaryota; Metazoa; Che
Mammalia; Eutheria; Pr.
1 (bases 1 to 1629)
Lafont, M. and Perron, H
Patent: FR 2791140-A 1
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Submitted (21-DEC-2000) R&D,
L'Etoile 69280, France
                                                                                                                Perron, H.,
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                                                                              Location/Qualifiers
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Multiple sclerosis retrovirus particles and recombinant envelope trigger an abnormal immune response in vitro, by inducing polyclonal vbeta16 T-lymphocyte activation
Virology 287 (2), 321-332 (2001)
                                                                                                                                                                                                                                                                                                                                                           AF331500 mRNA Multiple sclerosis associated retrovirus recombinant envelope protein (env) mRNA, AF331500 GI:13310190
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Eukaryota; Metazoa; Chordata; Cr. Mammalia; Eutheria; Primates; Ca. 1 (bases 1 to 172918)
Birren, B., Linton, L., Nusbaum, C. Homo sapiens, clone RP11-15N10
Unpublished
2 (bases 1 to 172918)
Birren, B., Linton, L., Nusbaum, C. Anderson, S., Baldwin, J., Barna, N
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 Nusbaum,C.,
J., Barna,N.,
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                                                            Craniata; Ve Catarrhini;
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 Lander, E.,
Beda, F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Mar 2, 2000 this sequence control and repeatMasker: All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 2, 2000 this sequence version replaced gi:6970363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Riley R., Rogov P., Rothman D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J. Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                             be preserved.
                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 178000; agarose-fp Insert size: 169718; sum-of-contigs Quality coverage: 2.9 in Q20 bases; Quality coverage: 3.0 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator B1g Dye; 100% of re Assembly program: Phrap; version 0.960731 consensus quality: 142569 bases at least Q30 consensus quality: 156863 bases at least Q30 consensus quality: 164107 bases at least Q20
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6 10200: co
1 10300: gap o
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36: contig of 1320 b
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3: contig of 1502 bp
10 of 1502 bp
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Young,G., Zainoun,J., Zimmer,A. and
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101200 113199: gap of 100 bp
101200 113135: contig of 11936 bp in
113136 113235: gap of 11936 bp in
113236 132520: contig of 19285 br in
132521 132620: gap of
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132521 132620; gap of 100 bp
132621 150646; contig of 18026 bp
150647 150746; gap of 100 bp
150747 172918; contig of 22777.
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                                                                                                                                      clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-15N10"
/note="assembly_fragment"
10301. .12003
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80817: contig of
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53373: contig of 2224
53473: gap of 100 b
58170: contig of 4697
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46232: contig
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69283: contig of 5785 bp in length
883: gap of 100 bp
75177: contig of 579 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473: gap of 100 bp
58170: contig of 4697 bp
270: gap of 100 bp
63398: contig of 5128 bp
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19115:
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89553: contig of 8636 bp in
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24: gap of 100 hr
30780: -
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24794: contig of 3202 bp
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g of 3375 bp
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Drive, Cambridge, MA 02140, USA
Location/Qualifiers
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/codon_start=1
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/product="syrylin precursor"
/protein_id="AAF28334.1"
/protein_id="AAF28334.1"
/protein_id="AAF28334.1"
/db_xref="GI:6760401"
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/db_xref="GI:6760401"
/ranslation="MALPYHEFIFTVLLPSFTLTAPPPCRCMTSSSPYQEFLWRMQRP
GNIDAPSYRSLSKGTPTFTAHTHMPRNCYHSATLCMHANTHYWTGKMINPSCEPLRTTRT
TVCWTYFTQTGMSDGGGVQDQAREKHVEVISQLTRVHGTSSPYKGLDLSKLHETLRT
TVCWTYFTQTGMSDGGGVQDQAREKHVEVISQLTRWTPPYGIVCLPSGIFFVCGTSA
YRCLNGSESMCFLSFLWPDMTYTTEOLLYNVISKPRKRVPFLFFVCGALG
TGIGGITTSTQFYYKLSQELNGDMERVADSLTVTLODQLNSLAAVVLQARRALDLLTAE
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2235. .2357
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/db_xref="taxon:9606"
/clone="AJ172-2s"
/tissue_type="testis"
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/note="transmembrane-region
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Nucleic sequence and deduced protein seq
endogenous retroviral motifs, and their
Patent: WO 9967395-A 22 29-DEC-1999;
INST NAT SAMTE RECH MED (FR); PERIN JEAN
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/protein_id="Rc07392.1"
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1 (bases 1 to 2599)
2 Perin,J.P., Rieger,F. and Alliel,P.M. Nucleic sequence and deduced protein sequence far endogenous retroviral motifs, and their uses patent: WO 9967395-A 1 29-DEC-1999;
INST NAT SANTE RECH MED (FR): PERIN JEAN PIERRE FRANCOIS (FR); ALLIEL PATRICK M (FR)
                         cctgttcctgaacaatggaacaacttcagcacagaaataaacaccacttccgttttagta
                                                                                                CAAAACCCTACTAACTGTTGGATATGCCTCCCCTGAACTTCAGGCCATATGTTTCAATC
                                                                                                                                  CATACTCGCCTGGTAAGCCTATTTAATACCACCCTCACTGGGCTCCATGAGGTCTCGGCC
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agcaatactatagacaccagctcccaatgcatcaggtgggtaacacctcccacacga
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Cranlata; Ve Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 10499)
Perin,J.P., Rieger,F. and Alliel,P.M. Nucleic sequence and deduced protein seque endogenous retroviral motifs, and their us patent: wO 9967995-A 3 29-DEC-1999; INST NAT SANTE RECH MED (FR); PERIN JEAN P FRANCOIS (FR); ALLIEL PATRICK M (FR) FRANCOIS (FR); ALLIEL PATRICK M (FR) ELOCATION/QUALIFIERS

Ce 1. 10499
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Sequence
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Patent: WO
Avalon Pha
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Mammalia; Eutheria;
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Pharmaceuticals (US)
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Primates;
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                                                                      Score 1333.8;
Pred. No. 0;
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                                                   GTCGCCGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
                                                                                                                       ACAACCTCTACTCAGTTCTACTACAAACTATCTCAAGAACTAAATGGGGACATGGAACGG
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                                 Submitted (13-NOV-1996)
Genome Sequencing Cente
                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                        Direct Submission
                                                                  Waterston, R.
                                                                                     The sequence of H. sapiens Unpublished (1996)
St. Loui
e-mail:
                                                                                                                         (bases 1 to 56093)
         Department of Genetics, I
St. Louis, MO 63108, USA
                                                                             (bases 1 to 56093)
                                 Sequencing Center
sapiens@watson.wustl.edu
                                                                                                                                                                                                               56093 l
RG083M05 from
                     Washington
                                                                                                     BAC
                                                                                                                                                                                                                bp DNA
n 7q21-7q22,
                                                                                                                                     Craniata; Vertebrata; | Catarrhini; Hominidae;
                                                                                                    clone
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                      University
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                                                                                                                                                                                                                 complete sequence
                                                                                                                                                Euteleostomi;
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

SOURCE INFORMATION:

VECTOR: pr Selection: This clone is from the first release of the human BAC library. library contains cloned DNA from a human male fibroblast cell 9785K. For references see: Shizuya et al., Proc. Natl. Azad. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996). рвецо

chloramphenicol

NEIGHBORING

SEQUENCE INFORMATION:

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The orientation of H_RGORAMOR clone contains Location/Qualifiers
1. .56093 position of H_RG083M05; unknown. actual end is at

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/gene="WUSSC:H_RG083M05.1"
/note="match to human 5' EST
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/db_xref="GI:1669371"
/db_xref="GI:1669371"
/tref="GI:1669371"
/
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/clone_lib="CITB-978SK-B"
complement(838. .1131)
/rpt_family="ALU"
                                                                                                                                                                                                                                                                                                                                                            /rpt_
13878
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/note="match to human 3' EST H75782 (NID:g1049794), bases
287-444"
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/rpt_family="ALU"
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/rpt_family="L1"
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complement/fff
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9483. 9547,11631. 11773,11864. 12021,13131. 
14885. 14988,16349. 16546,16837. 16971) 
/gene="WUGSC:H_RG083M05.1" to peroxisome 
/note="ArPase; strong similarity to peroxisome 
blosynthesis protein PASI (PID:g1172019); coded 
human cDNA C04279 (NID:g1467530)"
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/rpt_family="ALU"
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GKDQLFSQPPVLRTASQEGCQELTQEQRDQLRADISIIKGRYRSQSGEDESMNQPGPI
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/gene="WUGSC:H_RG083M05.1"
/note="match to human 5' E
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/note="match to human 5' EST H41382 (NID:917434),
143-266"
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/gene="WUGSC:H_RG083M05.1"
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/note="match to human fetal brain 5' EST (NID:9970409), bases 1-255, and to human
                                                 /rpt_ram11y= 18667. .19235
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/note="match to human 5' E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(48787.
/rpt_family="ALU"
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/note="match to human 3' EST N29952 (NID:g1148472), bases 290-455, and 5' EST R12730 (NID:g765806)"
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47898. .48115
/note="match to human 5' EST H6
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/rpt_family="ALU"
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complement(40632.
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complement(38938. .39224)
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/note="Grail prediction, score =
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/rpt_family="ALU"
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19550. .19670
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1148458), sequences are from opposite
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                                         aatggctcttcagaatctatgtgcttcctctcattcttagtgccccctatgaccatctac
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Tissue Procurement: ATCC
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                                                                                                                               High quality sequence stop: Location/Qualifiers
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        /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.5 kb. Library prepared by Life Technologies."
                                                    /clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:493894"
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Pan troglodytes DNA, clone: PTB-120G11.R, genomic su AG113694
AG113694.1 GI:16734213
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB PAR troglodytes male lymphoblast DNA, clone_lib:PTB PAR Library clone:PTB-120G11.R.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Unpublished
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Totoki, Y., Watanabe, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="PTB-120G11.R"
/Sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee M
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/db_xref="taxon:9598"
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                                                                                                                                                         tcagagagctcactaaaatgctaatcaggcaaaaacaggaggtaaagcaatagccaatca 725
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                                                                                                                                           TCGNAGAGCTCACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes DNA, clone: PTB-147110.R, AG134524.1 GI:16664202 GSS; GSS (genome survey semianon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiyama, A., Hattori, M., To
Totoki, Y., Watanabe, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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BAC end sequences of Library PTB
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troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male Library clone:PTB-147IIO.R.
                                                                                                                                                                                                                                                                                                 160
                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Site 1
R.Site 2
                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tracking errors.
                                                                                                                                                                                                                                                                                           /clone="PTB-147I10.R"
/sex="male"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
/clone_lib= "PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                        /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                     35.8%;
89.6%;
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SacI
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                                                                                                                                                                                                                     Score 475.2; DB 12; Pred. No. 1.9e-125;
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toyoda,A., Taylor,T.D., Yada,
nd Sakaki,Y.
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AG049953
Pan troglodytes DNA, clone:
AG049953
                                                                                                                                                                                                 and Chemical Research (RIXEN), Genomic Sciences Center (GSC);
1-7-25 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@sgc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC en
                                                                                                                                                                                                                                                                              Submitted (02-AUG-2001) Asao Fujiyama,
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                             Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                        BAC end sequences of Library PTB
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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GSS; GSS (genome survey
Pan troglodytes male lyn
                                                                                                                                                                    clone tracking
                                                                                                                                                                                   was generated during the R&D process
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troglodytes male lymphoblast DNA,
Library clone:PTB-030D19.F.
                                                                                                            Vector
                                                                                                                                      Sequencing: -21M13
                                                                              R.Site 1
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-030D19.F"
                                                            Location/Qualifiers
                                                .669
                                                                            : pKS145
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: SacI.
                                                                                                                                                                      errors.
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Best Local Similarity
Matches 548; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                          agcaacagcaacccctttgggtcccctcccattgtatgggagctctgttttcactctat 848
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                                                                                                                                                                                                                                                                                                                CGTCCTAATCGAGCTGAACACTAGTCACTGGGTTCCATGGTTCTCTTCCGTGACTCATGG
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                                                                              Pan troglodytes DNA, clone: PTB-124K18 AG116971
AG116971 GI:16737490
GSS: GSS (genome survey sequence)
Pan troglodytes male lymphoblast DNA,
BAC Library clone: PTB-124K18.F.
    Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB Unpublished
                                                   Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
                                                                        Pan troglodytes
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
/clone_lib="173 t
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Pred. No. 4.1e-125;
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                                 Taylor, T.D.,
                                                                                          clone_lib:PTB
                                                              Vertebrata;
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                                                              Euteleostomi;
                                                                                          Chimpanzee
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671 gagctcactaaaaatgctaatcaggcaaaaacaggaaggtaaagcaatagccaatcatctat 730
ccactcccgatcaggctaaaggcttgccattgttcctgcatggctaagtgcctgggtttg 1088
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                                                                                  CACTCTATTAAAATCTTGCAACTGCACTCTTCTTGGTCCGTGTTTTGTTATGGCTCAAGCT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cactctattaaatcatgcaactgca--ctcttctggtccgtgttttttatggctcaagct 908
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                                                                                                                                                                                                                                                                                                                                 CCATCCCTCCAGATCTGGCAGGGTGTCCACTGTGCTCCTGATCCAGCGAGGCGCCCATTG
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                                                                                                                                                                                                                                                  CCGCTCCCGATAGGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAACTGCCCAGGTTCA 495
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Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Fujlyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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R.Site 2
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee
/clone_154 g 165 t
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/db_xref="taxon:9598"
/clone="PTB-124K18.F"
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Pred. No. 8e-125;
0; Mismatches 5
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ACCESSION
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Best Local S
Matches 561
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| 676 CATTTT |
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                           cactctattaaatcatgcaactgcactcttctggtccgtgtttttttatggctcaagctga
                                                                  tgcctgagagcacagcgggaaggacaaggattggggatataaactcaggcattcaagccag
              TGCCTGAGAGCACAGTGGGATGGACAATGACCAGGATATAAACCCAGGCATTCCAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS; GSS (genome survey sequence). Pan troglodytes male lymphoblast DNA, BAC Library clone:PTB-097K23.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Totoki,Y., Watanabe,H. and
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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Totoki, Y., Watanabe, H. a
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Pan troglodytes DNA, clone:
AG096341
AG096341.1 GI:16716858
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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R.Site 1 : SacI
R.Site 2 : SacI.
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/clone_lib="PTB Chimpanzee Male
215 c 162 g 165 t
                                                                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-097K23.F"
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85.1%;
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Pred. No. 7.7e-124;
0; Mismatches 65;
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PTB-097K23.F,
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                                                                                                                                                                                                                                                                                                   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC en was generated during the R&D process and may have higher chance of clone tracking errors.
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GSS; GSS (genome survey
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Pan troglodytes DNA, clone:
AG072852
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Totoki, Y., Watanabe, H. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                     R.Site 1
R.Site 2
                                                                                                                                                                                                                                                            Sequencing: M13Rev
                                                                                                                                                                                                                             Vector
/clone="PTB-064H14.R"
/Sex="male"
/Sex="lymphoblast"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
/clone_lib="157 g 170 t
                                                                                                       /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                 location/Qualifiers
                                                                                                                                                . 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori,M., Toyoda,A., Taylor,T.D., atanabe,H. and Sakaki,Y.
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              Fujiyama, A., Hattori, M., Totoki, Y., Watanabe, H. a
                                                      Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y BAC end sequences of Library PTB
                                                                                                                    Pan troglodytes DNA, clone: PTB-102B0; AG099717
AG099717.1 GI:16720234
GSS; GSS (genome survey sequence)
Pan troglodytes male lymphoblast DNA, BAC Library clone: PTB-102B07.F.
Pan troglodytes
                                             Unpublished
                                                                                                         Pan troglodytes
Eukaryota; Metazoa;
                                                                                                  Mammalia; Eutheria;
                                                                                        (sites)
                                   (bases 1 to 712)
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Pred. No. 5.4
               ., Toyoda, A., Taylor, T.D., and Sakaki, Y.
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Catarrhini;
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al Similarity 87.28;
537; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Sushiro-chou. Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC enwas generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vector
R.Site 1
R.Site 2
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/clone_lib="PTB Chimpanzee
200 c 158 g 192 t
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/db_xref="taxon:9598"
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/sex="male"
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Pred. No. 1.2e-119;
D; Mismatches 66;
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                                                                                                                             CTGGACCAGCCTGCTAGCCCATGCTCTGATGTTAATGACATCGAAGGCACCCCTCCTGAG
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TCGTCGGCCAACCTCCCCAATGGCACTTGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGA
                                                               GAAATCTCAACTGCACAAACCCTTACTACACTCCAGTTCAGCAGGAAGCAGTTAGAGCGG
                                                                                                                                                                                                                                                                                                                       507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        689 bp DNA linear GSS 04-NOV-200 AG121669 AG121669 GSS: GSS 04-NOV-200 AG121669 L GI:16650834 GSS: GSS 7-7-1
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Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-130M15.F.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
159 c 176 g 189 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="PTB-130M15.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
/db_xref="taxon:9598"
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: SacI
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                                                                                                                                                                                                                                                                                                                                     Score 439.2;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                  rred. No. 4.2e-115;
: Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taylor, T.D., Yada, T.
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BH149565/c
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High quality sequence start: 40
High quality sequence stop: 567
Location/Qualifiers
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 921)
1 (bases 1 to 921)
1 Loftus,B., Wang,Z., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Ent
HM1:MSS sheared DNA library (2001)
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Dr., Tel: 301 838 0208 Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Brendan J Loftus
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                   242
     /Clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + 1 method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                  /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
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Direct Submission
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical submitted (Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                               Fujiyama, A., Hattori, M.,
Totoki, Y., Watanabe, H. a
                                                                                                         Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pan troglodytes DNA, clone: PTB-071A23.R, genomic su AG076758
AG076758.1 GI:16628560
GSS; Genome survey sequence).
GSS (genome survey sequence).
BAC Library clone:PTB-071A23.R.
                                                                                 Unpublished
                                                                                               BAC end sequences of Library PTB
                                                                                                                                                                   Pan troglodytes
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Primates;
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Pred. No. 6.3e-115;
0; Mismatches 84;
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and Sakaki,Y.
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Catarrhini;
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Pan troglodytes
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Query Match
Best Local Similarity
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                                                                                               gaccgcatccatctttaaacatggggcttgcaacttagctcacacccgaccaatcagaga
                                                                                                                                                                          agacaggactagctggatttcctaggctgactaagaatcccnaagcctanctgggaaggt 612
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                                                                                                                                                                                                                                       CGGTCGTCAGTCAACCTCCCCAGCAGCACTTGGGTTTTCCTGTTGAGAGGGGGGTACTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY
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/clone_lib="PTB Chimpanzee
157 c 187 g 171 t
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/db_xref="taxon:9598"
/clone="PTB-071A23.R"
/sex="male"
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Pred. No. 4.6e-114;
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DNA,

clone:

3 bp DNA PTB-106G16.F,

genomic

GSS 03-NOV-2001 survey sequence.

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                                                                                                                                     atttcactctattaaatcatgcaactgcactcttctggtccgtgtttttttatggctcaag
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                                                                                                                                                                                                                                                  ccagcaacagcaaccccctttgggtcccctcccattgtatgggagctctgttttcactct
                                                                                                                                                                                                                                                                                                                               CTATTGCCTGAGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTTGAG
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CTGAGCTTTCACTTGCTGTCCACCACTGCTGTTTTGTTGCCATTGCAGACCCACCGCTGA
                                                                                                         ATTTCACTCTATTAAATCTTGCAACTGTGCTCTTCTGGTCCGTGTTTGTAATGGCTCAAG
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Polived Submitsein Sakaki, Y.

Direct Submitsein Sakaki, Y.

Direct Submitsein Sakaki, Y.

Direct Submitsein Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-106G16.F.
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Totoki, Y., Watanabe, H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/clone_lib="PTB Chimpanzee Male BAC Library"
186 c 167 g 167 t 1 others
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/db_xref="taxon:9598"
/clone="PTB-106G16.F"
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nd Sakaki,Y.
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                                                                                                   517;
                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Dr., Rockville, MD 20850

9712 1301 838 0200

Fax: 301 838 0208

Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seg primer: SP6
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Other_GSSs: RPCI11-165G20.TV
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Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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RPCI11-165G20.TJ RPCI-11
                                                                                                                                                                                                                                                                                                                                                             Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao, William Nierman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Map Building
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                                                                                                               Similarity
                                                                                                                                                                                        152
                                                                                                   Conservative
                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:7563139"
/db_xref="taxon:9606"
/clone="RPCI-11-165G20"
/clone_lib="RPCI-11"
                                                                                                                                                                                  /cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCIll Human Male BAC Library"
169 c 135 g 154 t
                                                                                                                                                                                                                                                                                                                                  1. .611
                                                                                                                                                                                                                                            /sex="Male"
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                                                                                                              32.4%;
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Primates;
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Pred. No. 1.2e-11
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2e-112;
5 62;
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AG086046.1 GI:16637848
AG085; GSS (genome survey s
Pan troglodytes male lymp
BAC Library clone:PTB-084
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                                                                                                                                                                            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
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Pan trogl
                                                                                                                                                                                                                                                   Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                         Sequencing: M13Rev
                                                                                                                                                                                                                                                                                           (bases 1 to 736)
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troglodytes male lymphoblast DNA, clone_lib:PTB
Library clone:PTB-084E11.R.
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                                             Vector
R.Site
R.Site
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 Location/Qualifiers
1. .736
/organism="Pan troglodytes"
                                             : pKS145
: SacI
: SacI.
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PTB-084E11.R,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 714)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K. Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C
                                                                         Homo sapiens
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RPCI11-64L19.TJ
                                                                                                                    AQ238712.1
                                                                                                                                 AQ2387
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/clone="PTB-084E11.R"
                                                                                                                       GI:3671003
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Pred. No. 2.
                                                                                                                                                              714
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and Venter, J.C.

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Unpublished (1998)
Other_GSSS: RPC111-64L19.TK
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                 ACTCTTCTGGTCCATGTTTGTTCCGGCTCAAGCTGAGCTTTTGCTCGCCGTCCACCACTG
                                                                                                                                                                                                                                                                                                          ATGATCGGGATATAAACCCAGGCATTTGAGCCAGATCAGGTAACCCTCTTTGGGTCCCCT
CCATTGTTCCTGCACAGCTAAGTGCCTGGGTTCATCCTAATCAGGCTGAACACTGTTCGC
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Class: BAC ends.
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/db_xref="GDB:7524474"
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	AND POLYNUCLEOTID 928A 928A 31.8; DB 4; Len o. 3.7e-240; atches 69; Ind	
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                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                     APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 71
                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-POS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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APPLICATION NUMBER: FILING DATE:
                                                                                                                                          COUNTRY:
                                                                                                                                                         STREET: 87 Cambi
CITY: Cambridge
STATE: Massachus
                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                         Massachusetts
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87 CambridgePark Drive
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Lavallie,
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                                                                                                                                                                                                                                                                                                                                                                                                 Jacobs, Kenneth
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              US/08/686,878A
                                               Version
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RESULT 3
US-08-721-489-4
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Appli
Patent No. 578646
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ATTORNEY/AGENT INFORMATION:
NAME: BIOWN, SCOTT A.
REGISTRATION UNMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                            APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED
TITLE OF INVENTION: ENCODING
                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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CITY: Cambridge
STATE: Massachusetts
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CLASSIFICATION:
                                  APPLICATION NUMBER:
                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                        ADDRESSEE:
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02140
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Similarity 85.1%;
                 DATE:
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                                                                                                                                                                                                                                     E: Genetics Institute,
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                      McCoy, John
LaVallie, Edward
Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jacobs, Kenneth
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                                                                    PatentIn Release #1.0,
                                  US/08/721,489
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Pred. No. 2.4e-61;
1; Mismatches 38
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 58, Application US/08691563C
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                      SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,56:
                                                                                                                                                                                                                               APPLICANT: Florence KOMURIAN-PRADEL
APPLICANT: Colette JOLIVET
APPLICANT: Bernard MANDRAND
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
TITLE OF INVENTION: THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       ADDRESSEE: Oliff & Berridge
                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                       COUNTRY: U
ZIP: 22314
                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NTCANTAAAATGATNATTNGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
            FILING DATE:
                                                                                                                                                              STREET: 700 South CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RCCACATCCACCTTTAAACACGGGGNTTGCAAANAAGATNACACTTGACCAATCAGAGAG
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                                                                                                                                                 Virginia
                                                                                                                                                                         700 South Washington Street, Suite
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Frederic BEDIN
Glaucia PARANHOS-BACCALA
                                                                                                                                   U.S.A.
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               02-AUG-1996
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85.1%;
                           US/08/691,563C
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Pred. No. 2.4e-61;
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                                                      Version #1.30
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US-08-691-563C-46
US-08-691-563C-46; Sequence 46, Application US/08691563C; Patent No. 6001987; Patent No. 6001987
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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APPLICANT:
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les 333; Conserv
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         Frederic BESEME
Frederic BEDIN
Glaucia PARANHOS-BACCALA
Florence KOMURIAN-PRADEL
Colette JOLIVET
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                        agcagttagagcagttgtcagccaacctccccaacagtacttgggttttcctgttgagag
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: WP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
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FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
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ADDRESSEE: Oliff & Berridge
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STATE: Virginia
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                                                                                      TTCTACTGAGGACCCCTAGACCAACCCCCTGGCCCTTTCACTGGCCTAAAGAGTT-----
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                                                  gtcacccctcccgaggaaatctcaactgcacaacccctactacactccaattcagtagga 481
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                               CCCCTCTGGAGGACACTACCACTGCAGGGCCCCATCTTTGCCCCCTATCCAGAAGGA
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
THERAPEUTIC PURPOSES
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Pred. No. 4.6e-46;
D; Mismatches 247; Indels
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; ORGANISM: Nucleotide US-09-078-294-4
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CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 80246
TYPE: DNA
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Best Local Similarity
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APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
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                  agcagttagagcagttgtcagccaacctccccaaccagtacttggggttttcctgttgagag 541
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58.7%;
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Pred. No. 7.2e-44;
0; Mismatches 234
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; ORGANISM: Nucleotide sequence of HC-contig
US-09-078-294-3
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Best Local
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LENGTH: 80
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CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
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58.5%;
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Pred. No. 1.9e-40;
""smatches 214;
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US-08-007-282B-1
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                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                          1507
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NAME: MURPHY JR., GERALD M
REGISTRATION NUMBER: 28,977
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TITLE OF INVENTION: VACCINE COMPRISING FOWLPOX VIRUS
TITLE OF INVENTION: RECOMBINANTS EXPRESSING THE ENVE:
TITLE OF INVENTION: AVIAN RETICULOENDOTHELIOSIS RETRO
                                                                                                                                                                                             1447 CAGGAGAAGTGTTTTTTACGCTAACAAGTCGGGTATCGTACGTGACAAGATCCGAAAA 1506
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HYPOTHETICAL:
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                                                     1567 TTGAACGGCTTCCTTCCATATTTGCTACCCTTGTTAGGCCCCCTGTTTTGGGCTCATATTG
242 ttactcctctttggaccctgtatcttcaacttccttgttaagtttgtctctttccagaatt
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CITY: Falls Church
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                                                                        ctcagccaatggatgccctggactctccccttcttaggacctctagcagctataatattt
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CALVERT, JAY G.
WITTER, RICHARD L.
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US-09-011-745-8
; Sequence 8, Application US/09011745
; Patent No. 6165715
; GENERAL INFORMATION:
; APPLICANT: COllins, Mary KL
; APPLICANT: Weiss, Robin A
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, NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: n is any nucleotide
US-09-011-745-1
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APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PC7/GB96/02061
EARLIER FILING DATE: 1996-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: GB9
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: RD114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1990 caagaaaaatgctgtttttatgctaacaagtcaggaattgtgagaaacaaaataagaacc 2049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 2518
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                                                                                                                                                                                                      aatgttgtaca 2240
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APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER APPLICATION NUMBER: 398517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
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; LOCATION: (3802)
; OTHER INFORMATION: n is
US-09-011-745-8
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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LOCATION: (3801)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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LOCATION: (3614)
OTHER INFORMATION: n is
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NAME/KEY: misc_feature
LOCATION: (3613)
OTHER_INFORMATION: n is
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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NAME/KEY: misc_feature
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ctcagccaatggatgccctggactctccccttcttaggacctctagcagctataatattt 241
                                                                             atttgagatcgaatataatgtagagcagaggaccttcaaaacactgcaccctgggggcctc 181
                                                                                                                                                      ggggaagaatgctgttagtatgttaatcaatctggaatcattactgagaaagttaaagaa 121
                                                       caagaaaaatgctgtttttatgctaacaagtcaggaattgtgagaaacaaaataagaacc 2907
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Pred. No. 8.3e-17;
0; Mismatches 144;
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                                                                                                                                                           Matches
                                                                                                                                                                        Query Match 4.3%; Score 57; DB 1; Best Local Similarity 5.8%; Pred. No. 1.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                               1026
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                               PRIOR APPLICATION DATA:
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CTTY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                 TELL.
TELEFAX: (899149
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                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
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ttcactctattaaatcatgcaactgcactcttctggtccgtgttttttatggctcaagct 908
                                                          agcaacagcaaccccctttgggtcccctcccattgtatgggagctctgttttcactctat 848
                                                                                           4, Application US/08232463
5670367
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                                                                                                                                                         Conservative
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                     Length 7218;
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                                                                                                               Query Match
Best Local Similarity
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                                                                                                 Matches
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APPLICANT: Jay A. Fishman
                                                                                                                                                                                                                                                                                        TELEFAX: (617)227-594
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1266
                                  1619
                                                                                                                                                                                           TOPOLOGY: 1
MOLECULE TYPE:
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NAME: Louis Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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STREET:
STREET:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/572,645 FILING DATE: 14-DEC-1995
62 ggggaagaatgctgttagtatgttaatcaatctggaatcattactgagaaagttaaagaa 121
                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                             TYPE:
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                                                                                                                                                                                                                                                                                                                                                                    NAME: Louis Myers
REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                     : (617)227-7400
(617)227-5941
                                                                                                Conservative
                                                                                                                                                                                                            linear
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                                                                                                                              Score 50.8;
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Best Local Similarity
"~+~has 96; Conserv?
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Sequence 8, Application US/08258420 Patent No. 5710037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8132 base pairs
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA 08-766-528-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      7273 CTTAGAGAAAGGTTGGAGAAGCGTCGAAGGGAAAAGGAAACTACTCAAGGGTGG
                                                                                                                                                                                                                                      7153 CAGAATAGAAGAGGGTTAGATTTATTATTTCTAAAAGAAGGAGGATTATGTGTAGCCTTG 7212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                  122 atttgagatcgaatataatgtagagcagaggaccttcaaaacactgcaccctgg 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 atttgagatcgaatataatgtagagcagaggaccttcaaaacacctgcaccctgg 175
                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                          99998agaatgctgttagtatgttaatcaatctggaatcattactgagaaagttaaagaa 121
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Pred. No. 6e-06;
0; Mismatches 78;
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; NAME/KEY:
US-08-258-420-8
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Best Local Similarity
Matches 177; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
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SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                    1828
                                                                                                                      1768
                                                                                                                                                                                        1708
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LENGTH: 1911 bases
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                                                                                                                                                                                                                        179
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                                                                                    287
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STATE: New Jersey
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                                                                                                                  cagtccat 354
                                                   GTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTCAACAATATCACCAGCTG
                                                                                                                                                                                        GGGCTGTTTAATAGATCCCCCTGGTTTACCACCTTAATCTCCACCATCATGGGACCTCTA
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Pred. No. 2.1e-05;
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; TOPOLOGY: linear
; MOLECULE TYPE: genomic
US-08-258-420-9
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US-08-258-420-9
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Best Local Similarity 48.1
Matches 177; Conservative
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OPERATING SYSTEM: MS-DOS
SOFTMARE: WORDERCT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,420
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
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NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 27.
TELECOMMUNICATION INFORMATION:
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CTATE: New Jersey
rrqA
                                           1822
                                                                                                                                                                                                                                                       1642 AAAGAAGAATGTTGTTTTATGCAGACCACACGGGGCTAGTGAGAGACAGCATGGCCAAA 1701
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LENGTH: 1965 bases
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APPLICANT: Vanin, Elio F.
TITLE OF INVENTION: No. 5710037el Retroviral Envelope and LTR and Retroviral Vector
                                                                                                                                                                                   1702 TTAAGAGAAAGGCTTAATCAGAGACAAAAACTATTTGAGACAGGCCAAGGATGGTTCGAA 1761
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
                                                                                                           1762 GGGCTGTTTAATAGATCCCCCTGGTTTACCACCTTAATCTCCACCATCATGGGACCTCTA 1821
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MEDIUM TYPE: 3.5 inc
                                                                                                                                                     179
                                                                                                                                                                                                           122 atttgagatcgaatataatgtagagcagaggaccttcaaaacactgcaccctggggc--- 178
287 gtctcttccagaattgaagctgtaaagctacaaatagttcttcaaatggaaccccagatg 346
                                                                                                                                                                                                                                                                             62 ggggaagaatgctgttagtatgttaatccaatctggaatcattactgagaaagttaaagaa 121
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ZIP: 07068
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                                     ATAGTACTCTTACTGATCTTACTCTTTGGACCTTGCATTCTCAATCGATTAGTCCAATTT 1881
                                                            6 Becker Farm
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Pred. No. 2.1e-05;
0; Mismatches 176;
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Db 1882 GTTAAAGACAGGATATCAGTGGTCCAAGCTTTTGACTCAACAATATCACCAGCTG 1941
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Db 1942 AAGCCTAT 1949

Search completed: June 20, 2002, 09:40:25 Job time: 8535 sec

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Result
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Maximum DB seq length: 2000000000
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Best Local Sin
Matches 1329;
                                                                                                                                                                                                                                                                                                                                                                            related virus type 1 (MSRVI). The sequence can be used in diagr prophylactic or therapeutic compositions to inhibit expression multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis.
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P-PSDB;
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DB; AAW99554.
                                aagcagttagagcagttgtcagccaacctccccaacagtacttgggttttcctgttgaga
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             accaatcagagagctcactaaaatgctaatcaggcaaaaacaggaggtaaagcaatagcc
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       accaatcagagagctcactaaaatgctaatcaggcaaaaacaggaggtaaagcaatagcc
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(HYSE-) HYSEQ
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                                                                                                                                                                               chromosome
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2000US-0649167
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 INC.
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medical im
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Best Local Similarity
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   ccccctttgggtcccctcccattgtatgggagctctgttttcactctattttcactctatt
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24 - FEB - 2000

24 - FEB - 2000
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ve disorder; Crohn's disease; lymphoma;
deficiency syndrome; AIDS; autoimmune d:
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15-MAY-2000;
16-MAY-2000;
16-MAY-2000;
16-MAY-2000;
                                                                                                                                                                                   its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies against DITHPs and in assays to identify modulators of DITHP expression and activity. The anti-DITHP antibodies and antagonists may also be used to down regulate expression and activity. The anti-DITHP antibodies and antagonists may also be used as diagnostic agents for detecting the presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAS30986-AAS31196 represent human diagnostic and therapeutic (DITHP) polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                            The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and receptors (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate DITHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPs, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder, crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, leukaemia, autoimmune disorders, and respiratory disorders. Additionally, (I) may be used to produce the DITHPs, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) and
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DB; AAU19431.
                gaagctgtaaagctacaaatagttcttcaaatggaaccccagatgcagtccatgactaaa 361
gaagctgtaaaactactaattgttcttcaaaaggagccccagatgcagtccatgactaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eotides encoding diagnostic and therapeutic proteins, e.g. hormones and receptors, useful in diagnostics and therapeutics
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                                                            tcaaaatcgaagagctttagacctgctaaccgccaaaagagggggaacctgtttatttt
     aggagaagaacgctgttattatgttaatcaatccagaattgtcactgagaaagttaaaga
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21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotides isolated from human adult testes, adult brain, adult blood or adult placenta, or murine adult bone marrow or thymus cDNA libraries. The products of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemostatic activiny/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, and tumour inhibition activity. The polynucleotides are also stated to be useful
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             aatctaccgtggacccctggaccggcctgctagactatgctctgatgttaatgacattga
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DB; AAYO8622.
                                               gctactcctcttggaccctgtatctttaacctccttgttaactttgtctcttccagaat
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Matches Query Match Best Local (

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Conservative

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The invention relates to isolated polynucleotide (I) and CD polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags CC polynucleotides are also used in diagnostics as expressed sequence tags CC (II). (II) is useful in gene therapy techniques CC (II). (II) is useful in gene therapy techniques CC (II). (II) is useful in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical consideration of sites expressing (II). (I) and (II) are useful for treating CC imaging of sites expressing (II). (I) and (II) are useful for treating CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC and no acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed content for the problem of the problem of the problem of the printed of the problem of the printed of the problem of the problem of the printed of the problem of the proble
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                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid sequences from human endogenous retrovirus-Wexpressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnance
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dependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes associated with this susceptibility.
                                                                                                                                                                                                               This sequence represents clone cl.C4C5 of the human endogenous retreated. The nucleic acids, their fragments or peptides or by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulir
                                                                                                 Sequence 1136
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents an endogenetic retroviral nucleic acid fragment, which is associated with an autoimmune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 46; 53pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid from human endogenous retrovirus, useful e.g. diagnosis of autoimmune disease and complications of pregnancy contains at least part of the gag gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid sequences from human endogenous retrovirus-W expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnand
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                                       The present sequence represents an endogenetic retroviral nucleic acid fragment, which is associated with an autoimmune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell proliferation in vitro.
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selection:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      confirmed by restriction digest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Genetics, Washington
St. Louis, MO 63108, USA
e-mail: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                               clone
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/rpt_family="ALU" complement(6581.
                         complement(4948.
                                                                                                                                                                /protein_id="AAB46346.1"
/db_xref="GI:1669371"
                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               contains STS swSS1725
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RG083M05
University
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This sequence may not represent the entire insert of this It may be shorter because we only sequence overlapping once, or longer because we provide a small overlap between e only sequence overlapping provide a small ~~~ between

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was

This clone is from the first release of the human BAC library. Library contains cloned DNA from a human male fibroblast cell 1978K. For references see: Shizuya et al., Proc. Natl. Acad. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996). line

The orientation of this clone is unknown. clone is at base position 1 of H_RG083M05; of H_RG083M05 Actual start of this actual end is at 560 at 56093

/Clone="H_RG033M05"
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/Clone=11b="CITB-9785K-B"
/Clone=11b="CITB-9785K-B"
/Clone=11b="CITB-9785K-B"
/Complement(838. .1131)
/rpt_family="ALU"
<1360. 16971
/gene="WUGSC:H_RG083M05.1"
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14885. .14988.16349. .16546,16837. .16971)
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/Franslation-"KREWIQKTLEVAFSEAVWMQPSVVLLDDLDLLIAGLPAVPEHEH
/Franslation-"KREWIQKILEVAFSEAVWMQPSVVLLDDLDLIAGLPAVPEHEH
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MLLSKHSEILPDESKFNWYRLYFGSSYESLGANGTSSDLSGQCLSAPSSMTQDLPGVP
GKDQLFSQPPVLRTASQBGCQELTQEQRDQLRADISIIKGRYRSQSGEDESMNQPGPI
KTRLAISQSHLMTALGHTRPSISEDDWKNFAEL"

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/rpt_family="L1"
complement(15618.
/rpt_family="ALU"
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8473. 8675
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/note="match to human 5' ES
143-266"
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/note="match to multiple human ESTs, see N81064
(NID:g1243765), H48897 (NID:g988737), and M78831
(NID:g273146)"
                                                                                                                                                                                                                    complement(40247.
/rpt_family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                        /note="similarity to various SS-RNA virus polyproteins; pseudogene; region of matches and close matches to multiple human ESTs, see R68740 (NID:g842257)"
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/gene="WUGSC:H_RG083M05.1"

/note="match to human 5' EST

276-343"
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287-444"
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complement(8186. .
                                                                                                                                                                                        complement(40632.
/rpt_family="ALU"
                                                                                                                                                                                                                                                                                                                               /note="Grail prediction, score /evidence=not_experimental complement(38938..39224) //pt_family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(12612. .12907)
/rpt_family="ALU"
                                                                                          complement(45614. .45737)
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                                                                                                                          complement(45474.
/rpt_family="ALU"
                                                                                                                                                         complement(42283.
/rpt_family="ALU"
                                                                                                                                                                                                                                                                                vuote="match to multiple human (NID:g1148633)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match to human fetal brain 5' EST (NID:g970409), bases 1-255, and to human (NID:g759399)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match
21-348"
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/note="match to human 5' E
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/note="match to human 5' E
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                                                                                          H48898 (NID:g988738),
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3' EST
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Best Local Similarity
Matches 1133; Conserv
                                                                                                                                     37198
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                                                                                                                                                                     181
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                                                                                                                                                                                                                                                                                           61 aggggaagaatgctgttagtatgttaatcaatctggaatcattactgagaaagttaaaga 120
                                                                                                                                                                                                                                                                                                                                                             1 tcaaaatcgaagagctttagacttgctaaccgccaaaagagggggaacctgtttattttt 60
                                                                aatttgagatcgaatataatgtagagcagaggaccttcaaaacactgcaccctggggcct 180
                 tgaagctgtaaagctacaaatagttcttcaaatggaaccccagatgcagtccatgactaa
                                                                                                                                                                                                       AATTCGAGATCGAATACAACGTAGAGCAGAGGAGCTTCGAAACACTGGACCCTGGGGCCCT
                                                                                                                                                                                                                                                                         AGGGGAAGAATGCTGTTATTATGTTAATCAATCCGGAATCGTCACTGAGAAAGTTAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match to human 3 / EST N29952 (NID:g1148472) and 5 / EST N29938 (NID:g1148458), sequences are from opposite ends of the same clone" complement(49698. 51806) / gene="WUGSC:H_RG083M05.2" complement(join(49698. 49888,51575. 51806)) / gene="WUGSC:H_RG083M05.2" / note="coded for by human cDNAs W37389 (NID:g1319205), R65891 (NID:g838529), R65794 (NID:g838432) and R65794 (NID:g838432)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="ALG"
complement(47365.47782)
/note="match to multiple h
(NID:g1319089)"
47898.48115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (48406. .48584)
/note="match to human 3' EST N29952 (NID:g1148472),
290-455, and 5' EST N2730 (NID:g765806)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Grail prediction, score =
/evidence=not_experimental
complement(52052. .52329)
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/note="match to human 3'
309-440"
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/rpt_family="ALU"
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/rpt_family="ALU"
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93-368"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="WUGSC:H_RG083M05.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                           77.98;
                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 1035.2; DB 9; Pred. No. 6.1e-304; 0; Mismatches 111;
-CAAATGGAGCCCAAGATGCAGTCCAAGACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .49672)
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Direct Submission
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                                                                                                             CCACAGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGGTTCCATTCCTT-GAA
                                                                                                                                                       TGGGTTCATCCTAATTGAGCTGAACACTAGTCACTGGGTTCCATGGTTCTCTTCTGTGAC
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Best Local Similarity
Matches 1132; Conserv
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         ACCAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAGACAGGAGGTAAAGAAATAGCC
                   accaatcagagagctcactaaaatgctaatcaggcaaaaacaggaggtaaagcaatagcc
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Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1049)
Perin, J. P., Rieger, F. and Alliel, P.M.
Nucleic sequence and deduced protein sequence family endogenous retroviral motifs, and their uses Patent: WO 9967395-A 3 9-DEC-1999;
INST NAT SANTE RECH MED (FR); PERIN JEAN PIERRE (FR) FRANCOIS (FR); ALLIEL PARRICK M (FR)
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                Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Jöhnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulseged,H., Lozado,R.J., Lu,X., Lucler,A., Lucler,R., Luna,R.,
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1 (bases 1 to 188919)
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Homo sapiens chromosome 12 clone RP11-533J15, WORKING DRAFT
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Mapua, P.,
   Martin, R.,
   Martindale,A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (30-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 14, 2001 this sequence version replaced g1:12083977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'vorking draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-terminator Big Dye: 98% of reads
Chemistry: Dye-terminator Big Dye: 98% of reads
Chemistry: Dye-terminator Big Dye: 98% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 186874 bases at least Q40
Consensus quality: 189446 bases at least Q30
Consensus quality: 190585 bases at least Q20
Estimated insert size: 189222; sum-of-contigs estimation
Quality coverage: 8.2x in Q20 bases; sum-of-contigs estimation
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133018
133118
164867
164967
180053
180153
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Center clone name: RP11-533J15
----- Summary Statistics
Sequencing vector: plasmid; M77789
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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                                         /clone="RP11-533J15"
                                                                                                                 /organism="Homo sapiens"
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                                                                           /chromosome="12"
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61733: gap of unknown length
133017: contig of 71284 bp in length
133117: gap of unknown length
164866: contig of 31749 bp in length
164966: gap of unknown length
180952: contig of 15086 bp in length
180152: gap of unknown length
180919: contig of 8767 bp in length
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                                                                                  tcaggcattcaagccagcaacagc-aaccccctttgggtccccttcccattgtatgggag
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 AGACCCGCCACTGACTTCCATTCCTCTGGGTCCGGCAGGGTGTCCGCTGTGCTCCTGATC
                                         CCCAGGCATTCGAGCCGGCAATGGCTTACCCGCTTTGGGTCCCCTTTGTATGGGAG
                                                                                                                                                                          ACCAATCAGGTAGTAAAGACAGCTCAGTAAAAAGCTAGTTTGGCAAAAACAGGAGGTAAAG
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86.7%;
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COMMENT

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institu

Institute/ MIT Center for Genome

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RS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,M., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Liamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldiim,J., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldiim,J., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Pierre,N., J., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Pierre,N., J., Wallan,D., Ye,W.J., Pierre,N., and Zody,M.
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l (bases 1 to 161571)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-141A18
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC092708 161571 bp DNA linear Homo sapiens chromosome 18 clone RP11-141A18 map: SEQUENCE, 3 unordered pieces.
Submitted (20-JUL-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_DRAFT;
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FEATURES
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Best Local Similarity 88.6
Matches 1148; Conservative
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                                            CCTCAGCCAATGGATGCCCTGGATTCTCCCCCTTCTTAGGACCTCTAGCAGCTATAATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 32930: contig of 32930 bp in length
32931 33030: gap of 100 bp
33031 114301: contig of 81271 bp in length
114302 114401: gap of 100 bp
114402 161571: contig of 47170 bp in length
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Insert size: 161371; sum-of-contigs
Quality coverage: 9.8 in Q20 bases; agarose-fp
Quality coverage: 9.6 in Q20 bases; sum-of-contigs
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Chemistry: Dye-terminator Big Dye; 100% of read
Assembly program: Phrap; version 0.960731
Consensus quality: 160833 bases at least Q30
Consensus quality: 161352 bases at least Q30
Consensus quality; 161352 bases at least Q30
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CCATTTTGGAAGTGGCCTGCCATCTTGGGAGC
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CR Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., RS Birren, B., Landerson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Colengel, M., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Cohepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., EritzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Gyette, M., Graham, L., Jakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Karatas, A., Kells, C., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., McKernan, K., McPheters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McKernan, R., McKernan, K., McPhaelters, R., Maylor, J., Norbu, C., Norman, C., H., Murphy, T., Naylor, J., Noyen, C., Norbu, C., Norman, C., H., Norbu, C., Norman, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosettl, M., Royen, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Sovery, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Tropham, K., Travers, M., Traillio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zahnoun, J., Zembek, L., Zimmer, A., and Zody, M.
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Homo sapiens chromosome 18, clone RP11-2E13, complete sequence.
AC013759
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-JUN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 13, 2001 this sequence version replaced gi:14017510. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                   Center project name: L2525
Center clone name: 2_E_13
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                      Location/Qualifiers
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Best Local Similarity 88.6%;
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24660. .24769
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ement(32840
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                                                                                                                                                                                                                                                 Score 989.6; DB 9;
Pred. No. 4.9e-290;
0; Mismatches 117;
                                                                                                                                                                                                                                                 Indels 30; Gaps
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	. ccatttgggaagtggcccactgccattttggtagc 1280	1246	Qy
44088	CCTTGGAATCCATGAGGCCAAGAACCCCAGGTCAGAGAACACGAGGCTTGCCA	44029	Db
1245	.ccattccttggtatctgtgaggccaagaaccccaggtcagagaangtgaggcttgcc	1186	Qy
44028	CTCTTCCGTGACCCATGGCTTCTAATAGAGCTATAACACTCACT	43969	DЬ
1185	ttctcttccatgacccacggcttctaatagagctataacactcaccgcatggcccaaga	1126	Qy
9 1	GCATGGCTAAGTGCCCAGGTTCATCCTAATTGAGCTGAACACTAGTCACTGGGTT-CACA	9 6	Db 43
1 25	07#C07#################################	106	2
1065	ctgatccagcgaggtacccattgccactcccgatcaggctaaaggcttgccattgttcct	1006	, 4d VQ
43849	GCGCAGACCTGCCACTGACTTCCATCCCTTCGGATTCGGCAGGGTGTCCTCTGTGCCC	43790	Db
1005	ogtcacagaccogctgctgacttccatccctttggatccagcagagtgtccactgtgctc	946	Qy
43789		w	DЬ
945	tttttatggctcaagctgagcttttgttcgccatccaccactgctgtttgccac	891	Оу
43729	TCTGTTTTCGCTCTATTAAATCTTGCAACTGCGCTCTTCTGGTGCATG	43680	Db
890	ctgitttcactctatttcactctattaaatcatgcaactgcactcttctggtccgtg	833	Qy
43679	CCCAGGCATTCAAGCCAGCAATGGCTACCCTTTTGGGTCCCCTTTGTATTGGGAGC	43620	ДD
832	tcaggcattcaagccagcaacagcaaccccctttgggtcccctcccattgtatgggagc	773	Qy
43619	AAATAGCCAATCATCTTTCGCCTGAGACCACAGTGGGCGGGACAATGATCAGGATATAAA	43560	Дb
772	agccaatcatctattgcctgagagcacagcgggaaggacaaggattgggatataaa	713	ρ
43559	CCAACCAGGTAATAAGAGAGCTCACTAAAATGCTAATCAGGCAAAAAACAGCAGGTAAAA	43500	DЬ
712	tcagagagctcactaaaatgctaatcaggcaaaaacaggaggtaaag	661	Qy
43499	CTTTAAACATGGGGCTTGCAACTTAGCTCACACCGG	43440	DЬ
660	tgggaaggtgaccgcatccatctttaaacatggggcttgcaacttagctcacacccg	601	Qy
43439	GGGGGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACTAAGAATCCCTAAGCCT	43380	Db
600	ggtggactgagagacaggactagctggatttcctaggctgactaagaatcccnaagcct	541	Qy
ω	ANGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGCACCTTGGGTTTTCCTGTTGAGA	Ñ	Db -
540	caqttaqaqcaqttqtcaqccaacctccccaacaqtacttqqqtttttcctqttqaqa	481	Oy
43319		43260	Db
480	tcacccctcccgaggaaatctcaactgcacaacccctactacactccaattcagtagg	421	γQ
43259	ATGTTAATGACATCAA	43200	Db
420	tctaccgtggacccctggaccggcctgctagactatgctctgatgttaatgacattga	361	Qy
43199	GGTGTAAAGCTACAAATCATTCTTCAAATGGAGCCCCAGATGCAGTCCATGACTAA	43140	Дb
360	yaagctgtaaagctacaaatagttcttcaaatggaaccccagatgcagtccatgactaa	301	Ωу
43139		43080	Db
300	tactcctctttggaccctgtatcttcaacttccttgttaagtttgtctcttccaga	241	ρ
43079		43020	Db

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44089 CCATTTTGGAAGTGGCCTGCTGCCATCTTGGGAGC 44123

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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Only in DataBase (2000) In press 2 (bases 1 to 186911)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.
                                                                                                                                                                                                                                                                                                    preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Jul 14, 2000 this sequence version replaced gi:8117346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (E-mail:hattori@gsc.riken.go.jp, URL:ht
Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hattori, M., Ishii, K., Toyoda, A., Fujiyama, A., Yada, T., Totoki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hattori,M., Ishii,K., Toyoda,A., Fujiyama,A., Yada,T., Totoki,Y., Homo sapiens 186,911 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of Assembly program: Phrap; version 0.990329 Consensus quality: 182485 bases at least 040 Consensus quality: 184520 bases at least 030 Consensus quality: 185300 bases at least 030 Insert size: 185811; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: HumDraft18 Center clone name: RP11-693N15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                                                                                                                                            147462
164717
                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 9.41x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: RIKEN Genomic Sciences Center(GSC)
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164617 164716: gap of 100 bp
164717 171530: contig of 6814 bp in length
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91974 112096: contig of 20123 bp in
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17 91873: contig of
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186456. .186911
/note="assembly_fragment clone_end:SP6 vector_side:left"
38409 c 38950 g 53371 t 1100 others
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33209: gap of 100 bp
186355: contig of 3146 bg
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178451: contig of 6821
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132536: contig of 20340 bp in
32636: gap of 100 bp
147361: contig of 14725 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-APR-2000) to the DDBJ/EMBL/GenBank databases. Nobuyoshi Shimizu, Keio University, School of Medicine, Moleo Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail:nshimizu@dab.med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370)
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Shimizu, N., Kudoh, J. and Shibuya, K.
Direct Submission
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Shimizu, N., Kudoh, J. and Shibuya, K.
Homo sapiens genomic DNA, chromosome
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E 2 (bases 1 to 34000)

S Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Schudy,A.,
Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
Patterson,D., Reichmal,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G.,
Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
Reichelt,J., Kauer,G., Bloecker,H., Rammer,J., Beck,A., Klages,S.,
Hennig,S., Riesselmann,L., Dagand,E., Wehrmaeyer,S., Borzym,K.,
Gardiner,K., Nizetlic,D., Francis,F., Lehrach,H., Reinhardt,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-APR 2000) The Chromosome 21 Mapping and Sequencing Consortium: *RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * Genetics (addresses see below) On May 30, 2000 this sequence version replaced gi:7717295. The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagamihara 228-8555, Japan, * e.mail: hattoriggsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Park, H.S., Toyoda, A., Ishii, K., Totoki, Y., Choi, D.K., Soeda, E., Ohki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K., Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R., Patterson, D., Reichwald, K., Rump, A., Schillhabel, M. and Schudy, A. The DNA sequence of human chromosome 21. The chromosome 21 mapping and sequencing consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * Institute of Molecular Biotechnology, Genome Beutenbergstrasse 11, D-07745 Jena, Germany, e.mail: gscj-submit@genome.imb-jena.de
* e.mail: http://genome.imb-jena.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160-8582, Japan,
* e.mail: nshimizu@dmb-med.keio.ac.
                                                                                                                                                                                                                                                                                                                                                                                           info.genome@gbf.de
                                                                                                                                                                                                                                   Max-Planck Institute for Molecular Genetics, Ihnestrasse 73, D-14195 Berlin, Germany, e.mail: info-chr21@molgen.mpg.de URL: http://chr21.rz-berlin.mpg.de/L163242: Submitted (10-Apr-2000).
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Mascheroder Weg 1, D-38124 Braunschweig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keio University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            il: nshimizu@dmb-med.keio.ac.jp/
  http://www.dmb.med.keio.ac.jp/
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Best Local Similarity 88.5%;
Matches 1120; Conservative
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Pred. No. 8.1e-289;
0; Mismatches 122;
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Mammalia; Eutheria; Primates; Catarrhini;
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Shimizu,N., Kudoh,J. and Shibuya,K.
Homo sapiens genomic DNA, chromosome 21,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 172721)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
                                                                                                                       Homo sapiens
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                                                                                                                                                         HTGS_PHASE1;
                                                                                                                                                      GI:14190616
ASE1; HTGS_DRAFT.
                                                                                                                                                                                                         chromosome 12 clone unordered pieces.
                                                                                                                                                                                                                                           172721 bp
                                                                                                                                                                                                                         RP11-407N8, WORKING DRAFT
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JOURNAL REFERENCE

TITLE

AUTHORS TITLE

JOURNAL

COMMENT

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 20 contigs. The true order of the pieces
is not known and their order in this sequence record is

NOTE: Estimated insert size may differ from sequence length

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Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Cherker, M., Cawazos, S.R., Chacko, J.C., Chavel, J.C., Chen, R., Chen, C., Cheward, M., Charles, C., Chen, R., Chen, R.,
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ORIGIN
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Best Local Similarity 86.5%;
Matches 1158; Conservative
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                                                                                                                                                                                                                                                                              Location/Qualifiers
1.172721
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-407N8"
/a 34893 c 35040 g 50742
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156803:
156903:
160332:
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164479:
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303: contig o
403: gap of u
403: gap of u
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463: gap of u
563: gap of u
284: gap of u
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284: gap of u
670: contig o
671: contig o
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672: gap of u
672: gap of u
673: gap of u
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Pred. No. 6.6e-288;
0; Mismatches 157;
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g of 15621 bp in length
f unknown length
lg of 6174 bp in length
lg of 6174 bp in length
lg of 6174 bp in length
g of 7043 bp in length
g of 7087 bp in length
f unknown length
lg of 7091 bp in length
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lg of 5062 bp in length
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lg of 5866 bp in length
lg of 6866 bp in length
lg of 1867 bp in length
lg of 1867 bp in length
lg of 1868 bp in length
lg of 2074 bp in length
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                                                               240
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	2 aaggatcccccagtaaca 1329 	1312 40006	Оу
1311	2 gggaagtggcccactgccattttggtagcggcccaccatctttgggagctgtggggagc	1252	Db
40005		39947	Qy
1251 39946	2 tccttggtatctgtgaggccaagaaccccaggtcagagaangtgaggcttgccaccattt	1192 39888	ρδ
1191	ttccatgacccacggcttctaatagagctataacactcaccgcatggcccaagattccat	1132	Qy
39887		39828	Db
1131 39827	ctaagtgootgggtttgtootaatagaaotgaacaotggtoactgggttooatggttotc	1072 39768	οy
1071	2 cagcgaggtacccattgccactcccgatcaggctaaaggcttgccattgttcctgcatgg	1012	Qy
39767		39708	Db
1011	agacccgctgctgacttccatccctttggatccagcagagtgtccactgtgctcctgatc	952	dg
39707		39648	VQ
951	tttttatggctcaagctgagcttttgttcgccatccaccactgctgtttgccaccgtcac	892	QQ
39647		39588	db
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39359		39300	Db
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39299		39240	
540	aagcagttagagcagttgtcagccaacctccccaacagtacttgggttttcctgttgaga	481	Оу
39239		39180	
480 39179	agtcacccctcccgaggaaatctcaactgcacaacccctactacactccaattcagtagg	4 21 39120	Qу
420 39119	aatctaccgtggacccctggaccggcctgctagactatgctctgatgttaatgacattga	361 39060	Оу
360	tgaagctgtaaagctacaaatagttcttcaaatggaaccccagatgcagtccatgactaa	301	Qy
39059			Db

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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 27, 2000 this sequence version replaced gi:6466621. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tesfaye,S., Tirrell,A., Vassillev,H., vo Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
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1 (bases 1 to 145785)
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Center project name: L3813

Center clone name: 440_C_21

Center clone name: 440_C_21

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 136132 bases at least Q40
Consensus quality: 136172 bases at least Q30
Consensus quality: 141708 bases at least Q20
Insert size: 187000; agarose-fp
Ouality coverage: 3.6 in Q20 bases; sum-of-contigs
Ouality coverage: 4.6 in Q20 bases; sum-of-contigs
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
2628: contig of 1197
2629 2728: gap of 100 bp
2729 3745: contig of
3746 3845
                                                                                                               1332 1431: gap
1432 2628:
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                                                                                                                                                                                                                1331:
                                                                                                                                                                                                            contig of 1331 bp in
                                                                                                                             bp in length
                                     bp in length
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sum-of-contigs
                                                                                                                                                                                                            length
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Db	6951	6951 CAGACCCGTCGCTGACTTCCATCCCTCCAGATCTGGCAGGGTGTCCACTGTGCTCCTGAT 6892	92
Qy	1011	ccagcgaggtacccattgccactcccgatcaggctaaaggcttgccattgttcctgcatg 1070	70
DЬ	6891	CCAGCGAGGCACCCATTGCCGCTCCCAATCGGGCTAAAGCCTTGCCATTGTTCCTGCACA 6832	32
Qy	1071	gctaagtgcctgggtttgtcctaatagaactgaacactggtcactgggttccatggttct 1130	30
В	6831	6831 GCTAAGTGCCTGGGTTCGTCCTAATCAAGCTGAACACTAGTCACTGGGTTCCATGGTTCT 6772	72
Qy	1131	1131 cttccatgacccacggcttctaatagagctataacactcaccgcatggcccaagattcca 1190	90
Db	6771	6771 CTTCCATGACCCATGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCA 6712	12
Qy	1191	ttccttggtatctgtgaggccaagaaccccaggtcagagaangtgaggcttgccaccatt 1250	50
В	6711	TTCCTTGGAATCCGTGAGGCCAAGAACCCCCAGGTCAGAGAACACGAGGCTGCTGCCATCT 6652	52
Qy	1251	1251 tggga 1255	
В	6651	6651 TGGAA 6647	

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